

## STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number

TO: Nancy Vogel

Location: rem/2a70/2c70

Art Unit: 1636

Wednesday, May 11, 2005

Case Serial Number: 09/896888

From: Edward Hart

**Location: Biotech-Chem Library** 

**REM-1A55** 

Phone: 571-272-2512

edward.hart@uspto.gov

#### Search Notes

Examiner Vogel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 



Inspale Blonk Usolo)

#### STIC-Biotech/ChemLib

152272

From:

Vogel, Nancy

Sent: Vogel, Nailcy
Tuesday, May 03, 2005 7:14 AM

To:

STIC-Biotech/ChemLib

Subject:

sequence search for 09/896,888

please do sequence search of SEQ ID NO:1, nucleotides 351-527 of SEQ ID NO:1, and SEQ ID NO:10, including interference files,

of 09/896,888

and return results to me on paper asap.

Thanks

Nancy Vogel Patent Examiner Art Unit 1636 Office: Remson 2A70 Mail Box: Remson 2C70 (571) 272-0780

HAY - 3 2005

STAFF USE ONLY

Searcher: \_\_\_\_\_\_ Searcher Phone: 2-

Date Searcher Picked up:

Date Completed: Searcher Prep/Rev. Time:

Searcher Prep/Rev. Time Online Time:\_\_\_\_\_

Type of Search

NA#: \_\_\_\_ AA#: \_\_\_\_ Interference: \_\_\_ SPDI: \_\_ S/L: \_\_\_ Oligomer: \_\_\_ Encode/Transl: \_\_\_\_

Structure#:\_\_\_\_\_ Text:\_
Inventor:\_\_\_\_ Litigation:\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*
Vendors and cost where applicable STN:\_\_\_\_\_

DIALOG:\_\_\_\_\_

QUESTEL/ORBIT:\_\_\_\_\_LEXIS/NEXIS:\_\_\_\_\_

SEQUENCE SYSTEM: WWW/Internet: Other(Specify):

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## STIC SEARCH RESULTS

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

## Voluntary Results Feedback Form

| >   | I am an examiner in Workgroup: Example: 1610   |
|-----|--|
| >   | Relevant prior art found, search results used as follows:  |
|     | 102 rejection  |
|     | ☐ 103 rejection  |
|     | ☐ Cited as being of interest.  |
|     | ☐ Helped examiner better understand the invention.   |
|     | ☐ Helped examiner better understand the state of the art in their technology.                    |
|     | Types of relevant prior art found:   |
|     | ☐ Foreign Patent(s)  |
|     | Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.) |
| >   | Relevant prior art not found:  |
|     | Results verified the lack of relevant prior art (helped determine patentability).                |
|     | Results were not useful in determining patentability or understanding the invention.             |
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ARS27545 Sequence
M31883 Cloning vec
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THOMAS A GRIGIATTI, DAVE A THEILMANN, THOWAS
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HTCS. PHASEO
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* sequencing reads that have not been assembled into
* contigg. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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COMMENT

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S. [Linton, L., Winsbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Baddan, J., Castellano, K., Dewar, K., Oadlan, S., Collymer, A., Cooke, P., Dakzellano, K., Dewar, K., Oadlan, L., Martasa, A., Klein, J., Gardyna, S., Grant, C., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Rann, L., Karstas, A., Klein, J., Lehockky, J., Mister, C., Looker, K., Macdonald, P., Marquis, N., McGwarn, P., McGurran, K., McLaughlin, J., Meldrim, J., Ranger, T., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thoman, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wman, D., Ye, W.J., Zimmer, A. and Zody, M.

All Direct Submission

AL Subm
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 22, clone RP11-348B6
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------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows Contact: sequence\_submissions@genome.wi.mit.edu ------ Project Information NOTE: This record contains 124 individual Center clone name: 348 B 6 Center project name: L3764

AC013315 118229 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 22 clone RP11-348B6 map 22, LOW-PASS SEQUENCE SAMPLING.

DEFINITION

RESULT 3 AC013315

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3876 rrharrecerececreacrecececrirecaerececaaaecrere 3923

3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG

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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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AC013368 211967 bp DNA linear HTG 13-JUL-2000
HOmo sapiens clone RP11-11016, LOW-PASS SEQUENCE SAMPLING.
AC013368 GI:9123839
HTG; HTGS PHASEO.
Homo sapiens (human)
Homo sapiens (human)
Homo sapiens (human)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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| Sirren, B., Lincon, L., Nuchaum, C. and Lander, E.  10 House species of Corner FP1111016  2 Uniblishmed C. 21187)  2 Uniblishmed C. 21187)  2 Uniblishmed C. 21187)  2 Uniblishmed C. 21187)  2 Editor, A., Callange, E., Collymore, E. | 111222:<br>11222:<br>11880:<br>12640:<br>12740:<br>13500:<br>14240:<br>14240:<br>14840:<br>14876:<br>14876:<br>16390:<br>16390:<br>17143: | 100 bp in 100 bp | 35952: contig of<br>36052: gap of 100<br>36683: contig of<br>36783: gap of 100<br>37452: contig of<br>37552: gap of 100<br>38208: contig of                                       |
|--|---|--|---|
| AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT  | 2   | <b>₹</b>   | 8235: gap of 100 bp<br>8900: contig of 665 bp in<br>9000: gap of 100 bp<br>9652: contig of 652 bp in<br>9752: gap of 100 bp<br>10378: contig of 626 bp in<br>10478: gap of 100 bp |

Donelan, L., Doyle, M.,

Collymore, A.,

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Seearch, 320 Charles Street, Campringe, FM 02141, USA, Research, 320 Charles Street, Camber, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Bouchgalter, B., Brown, A., Bate, F., Colangelo, M., Catle, A., Choepel, Y., Colangelo, M., Collins, S., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Dodge, S., Domino, M., Doyle, M., Ferreita, P., FitzHugh, W., Gage, D., Grand, Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Ilievi, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazres, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McZarthy, M., McKan, P., McGurk, A., McKernan, K., McDheeters, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Meneus, L., Mihova, T., Miranda, C., Menega, V., Morrow, J., Norman, C.H., O'Connor, T., O'Donnell, P., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Scojanovic, N., Subramanian, A., Talamas, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wayman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M. Direct Submission

All Submitted (24-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M. Perreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., FatzHugh, W., Forrest, C., Funke, R., Gage, D., Gadagand, J., Gardyna, S., Grant, G., Hagos, B., Hedrord, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kamn, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGwan, R., McEwan, R., McLaughlin, J., Meldrim, J., Morrow, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Mheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                                Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This record contains 270 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Web site: http://www-seq.wi.mit.edu
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HOMO sapiens chromosome 18 clone CTB-155C15 map 18, LOW-PASS
SEQUENCE SAMPLING.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                         75: contig of 670 bp in length

7: gap of 100 km
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gap of 100 bp
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gap of 100 bp
contig of 668 bp in length
gap of 100 bp
contig of 637 bp in length
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of 642 bp in length
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 18, clone CTB-155G15 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.8; DB 2;
Pred. No. 0.0032;
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ad7 bp in length
y7: contig of 875 bp in length
77: gap of 100 bp
4: contig of 867 bp in
contig of 867 bp in
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contig of 872 bp in length
gap of 100 bp
contig of 877 bp in length
gap of 100 bp
contig of 880 bp in length
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contig of 889 bp in length
gap of 100 bp
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gap of 100 bp
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1 (bases 1 to 73282)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone 1 E 17

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Homo sapiens clone RP11-337M23, LOW-PASS SEQUENCE SAMPLING.
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(Cypriniformes; Cyprinidae; Danio.

(Chases I to 604)

Shimoda,N., Knapik,E.W., Ziniti,J., Sim,C., Yamada,E., Kaplan,S., Jackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.

Zebrafish genetic map with 2000 microsatellite markers

Genomics 58 (3), 219-232 (1999)
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Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishman@mgh.cvrc.harvard.edu
Primer A: CACCGAGCTTCACTGACGTA
Primer B: ATACACACCCAAGCCGACAT
STS size: 112
PCR Profile: 94 degrees C for 5.0 minutes
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Pred. No. 0.0054;
); Mismatches 8; Indels 0;
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Annealing:
Polymerization: 7
PCR Cycles: 2
Thermal Cycler: M
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Best Local Simi
Matches 41;
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AUTHORS
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C12P21/02/C12Q1/03,
PC C12Q1/68,G01N33/15,G01N33/59,G01N33/56,G01N33/68,PC C12Q1/68,G01N33/15,G01N33/50,G01N33/59,G01N33/59,PC C12N15/00,
PC C1 equals a,t,g, or c
PC n equals a,t,g, or c
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1 (bases 1 to 826)
Shimoda,N., Knapik,B.W., Ziniti,J., Sim,C., Yamada,B., Kaplan,S., Jackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C. Eberafish genetic map with 2000 microsatellite markers Genomics 58 (3), 219-232 (1999)
                                                                                                                            AGIP21/04,

AGIP25/00, AGIP25/14, AGIP25/16, AGIP25/28, AGIP25/30, AGIP27/02,

AGIP27/00, AGIP29/00, AGIP31/04, AGIP31/10, AGIP31/12, AGIP31/18,

AGIP33/00,

AGIP33/00,

AGIP33/00,

AGIP33/00,

CO7K14/47, CO7K16/18, CI2N1/15, CI2N1/19, CI2N1/21, CI2N5/10 PC
                                                       PC A61P9/06,A61P9/08,A61P9/10,A61P9/12,A61P9/14,A61P11/00 PC
,A61P11/06,A61P13/02,
PC A61P13/12,A61P15/00,A61P17/02,A61P17/06,A61P19/02,A61P21/00,
              A61P1/16, A61P3/10, A61PS/00, A61P7/02, A61P7/04, A61P7/06, A61P7/08,
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Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishmandengh.cvrc.harvard.edu
http://sebrafish.mgh.harvard.edu
primer A: CACATGTGGACCGGACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ce 1. 745 /organism='Homo sapiens (human)'. Location/Qualifiers
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83.3%; Pred. No. 0.0067;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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27956 Zebrafish AB Danio
G40613
G40613.1 GI:3359822
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/organism="Homo
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Matches 40; Conservative
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CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
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1 (bases 1 to 745)
Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Moore,P.A., Komatsoulis,G. and Birse,C.E.

33 human secreted proteins
Patent: JP 2002534972-A 36 22-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.6%; Score 35.8; DB 11; Length 604; ilarity 83.3%; Pred. No. 0.0067; Conservative 0; Mismatches 8; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562
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                                                                                                                                                                                                                                            Primers are available from Research Genetics Inc.
                                                                                                                                                                                                                                                               (http://www.resgen.com_phone: 800-533-4363)
Location/Qualifiers
                                                                                                                         1.5 mM
50 mM
10 mM
8.3
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each 200 uM
0.034 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Zebrafish AB"
/dev_stage="Adult"
/lab_host="DH5alphaF'IQ"
                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="AB"
                                                                                                                                                                                                                                                                                                                                        organism="Danio rerio"
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19-JAN-1999 US 60/1163:
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complement (280. .299)
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BD269301
                                                                                                                                             KCl:
Tris-HCl:
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JP 2002534972-A/36
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JP 2002534972-A/36.
Homo sapiens (human)
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       dNTPs:
Taq Polymerase:
Total Vol:
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Best Local Similarity
Matches 40; Conserv
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primer_bind.
ORIGIN
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AUTHORS
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Gaps

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/dev stage="Adult"
/lab_host="DH5alphaP'IQ"
/lab_host="Vector: ml3MP19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with AluI, Cac8I, HaeIII, NlaVI, or
RsaI. Fragments in the range of 250-500 bp were gel ,
purified and a BstXI linker was added. The fragments were
cloned into a modified Ml3Mp19 vector and transformed
into B. Coli DH5alpha. Microsatelllite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                            Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Pax: 6177265806
Zebrafish genetic map with 2000 microsatellite markers
Genomics 58 (3), 219-232 (1999)
99303552
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                                                                                                                                                                                                                                                                                                                         94 degrees C for 5.0 minutes 94 degrees C for 1.0 minute 58 degrees C for 1.0 minute 72 degrees C for 1.5 minute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              are available from Research Genetics Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phone: 800-533-4363)
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50 mM
10 mM
8.3
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Pred. No. 0.0068;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                            MJ Research PTC-100
                                                                                                                                                                                                Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: TCAATCTGAAACTCGGA
Primer B: CGCTTTATAGGGCTGCAGG
STS size: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.034 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone lib="Zebrafish AB"
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each 200 uM
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/organism="Danio rerio"
/mol_type="genomic DNA"
/strain="AB"
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/map="LG 16"
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complement (344. .363)
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PCR Cycles:
Thermal Cycler:
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                                                                                                                                                                                                                                                                                                                                                  Denaturation:
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Best Local Similarity
Matches 40; Conserval
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/dev stage="Adult"
/lab_nost="DHSalphar'IQ"
/lab_nost="DHSalphar'IQ"
/lab_nost="DHSalphar'IQ"
/note="Vector: mi3MP19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with Alu!, Cac81, HasII, NINIV, or
Rsal. Fragments in the range of 250-500 bp were gel
purified and a BstX1 linker was added. The fragments were
cloned into a modified Mi3mp19 vector and transformed
into B. COli MBSalpha. Microsatelllite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
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220177 Zebrafish AB Danio rerio STS genomic, sequence tagged site.
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Danio rerio
Danio rerio
Bukaryora retacos, Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
I (bases I to 979)
Shimoda, N., Knapik, E.W., Ziniti, J., Sim, C., Yamada, E.; Kaplan, S., Jackson, D., de Sauvage, F., Jacob, H. and Fishman, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
71.6%; Score 35.8; DB 11; Length 826;
Best Local Similarity 83.3%; Pred. No. 0.0068;
Matches 40; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 TTAANTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primers are available from Research Genetics Inc.
                                                            94 degrees C for 5.0 minutes 94 degrees C for 1.0 minute 58 degrees C for 1.0 minute 72 degrees C for 1.5 minute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.resgen.com_phone: 800-533-4363)
Location/Qualifiers
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50 mM
10 mM
                                                                                                                                                                 MJ Research PTC-100
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each 375 nM
each 200 uM
0.034 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'mol_type="genomic DNA"
'strain="AB"
  Primer B: TCTCTCCCCTGGACATCATC
STS size: 142
PCR Profile:
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/map="LG 16"
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Tris-HCl:
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Polymerization: 7
PCR Cycles: 2
Thermal Cycler: M
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SOURCE
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AUTHORS
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Gaps

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we: contig of 760 bp in length 36: gap of 100 bp 1: contig of 760 bp in length 1: contig of 775 bp : gap of 100 tp 100 tp
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+: contig of 798 bp in length

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ACUZIS42 76295 bp DNA linear HTG 13-JUL-2000 SEDIENCE SAMPLING.
                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases, Linton,L., Nusbaum,C. and Lander,E. Homosapiens chromosome 15, clone RP11-165P21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission.
Submitted (15-FBB-2000) Whitehead Institute/MIT Center for Genome Submitted (15-FBB-2000) Whitehead Institute/MIT Center for Genome Steesarch, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6978228.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
rarbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
_------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 788 bp in length gap of 100 bp
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Center clone name: 165_P_21
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Homo sapiens (human)
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Dupublished

S (bases I to 75002)

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barnan, N., Bada, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Devare, K., Dodge, S., Domino, M., Doyle, M., Garelano, C., Gage, D., Fenestor, J., Ferreira, P., Fizidhy, W., Forrest, C., Gage, D., Grand-Pierre, N., Grand, G., Hadford, A., Horton, L., Fenestor, J., Langorque, K., Lehoczky, J., Levine, R., Kiein, J., Langorque, K., Lehoczky, J., Levine, R., Kiein, J., Locke, K., McGard, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Meheeters, R., Meldrim, J., Mihova, T., Mihova, T., Minanda, C., Menga, V., Morrow, J., Naylor, J., Norman, C. H., O'Comnor, T., O'Donnell, P., O'Nell, D., Olivar, T. M., Severy, R., Spencer, B., Stange-Thomann, V., Raymond, C., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Trayers, M., Trigillo, J., Vaung, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 75002)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens chromosome 11 clone RP11-589112 map 11, LOW-PASS
SEQUENCE SAMPLING.
                                                       Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 01709/9-A 13142 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
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/mol_type="unassigned DNA"
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html All repeats were identified using RepeatMasker: Center code: WIBR Web site: http://www-seq.wi.mit.edu

Homo sapiens (human)

DEFINITION

RESULT 13 CQ406071

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ACCESSION VERSION KEYWORDS

Homo sapiens

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L. Submitted (07-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
L. Hutp://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95127)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-1015
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Center: Whitehead Institute/ MIT Center for Genome Research
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Homo sapiens clone RP11-1J15, LOW-PASS SEQUENCE SAMPLING.
AC016798
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                    ;
                                                                                                                                             Score 35.6; DB 2; Length 75002;
Pred. No. 0.009;
0; Mismatches 9; Indels 0;
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------ Project Information
Center project name: L2499
contig of 772 bp in length
gap of 100 bp
contig of 721 bp in length
gap of 100 bp
contig of 744 bp in length
gap of 100 bp
contig of 748 bp in length
contig of 748 bp in length
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 Query Match
 71.2%;
 Score 35.6;
 DB 2;
 Length 95127;

 Best Local Similarity 82.0%;
 Pred. No. 0.0091;
 Matches 41;
 On Gaps 0;

 Matches 41;
 Conservative 0;
 Mismatches 9;
 Indels 0;
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Search completed: May 10, 2005, 05:52:47 Job time : 306.908 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Aav62498 Plasmid p<br>Aas89978 DNA encod | Aas92596 DNA encod<br>Aaa87692 Human sec | Acn86091 Breast ca | Acn83021 Breast ca | Aaf55360 Sequence | Adl39252 Human ova | Aas77556 DNA encod | Aas77545 DNA encod | Aas69138 DNA encod | Aas77547 DNA encod | Aas87523 DNA encod | Aas77561 DNA encod | Ade09733 Novel DNA | Aas69873 DNA encod | Ade48102 Human che | Aas69432 DNA encod | Aas85906 DNA encod | Aas92595 DNA encod |
|-------------------------------|--|--|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES                     | AAV62498<br>AAS89978                     | AAS92596<br>AAA87692                     | ACN86091           | ACN83021           | AAF55360          | ADL39252           | AAS77556           | AAS77545           | AAS69138           | AAS77547           | AAS87523           | AAS77561           | ADE09733           | AAS69873           | ADE48102           | AAS69432           | AAS85906           | AAS92595           |
| 0B                            | <b>61</b> 12                             | n u                                      | 1                  | 1                  | 4                 | ß                  | S                  | Ŋ                  | S                  | S                  | Ŋ                  | S                  | 10                 | 2                  | 12                 | Ŋ                  | ß                  | S                  |
| %<br>Query<br>Match Length DB | 50<br>16091                              | 20795                                    | 791                | 869                | 327               | 586                | 1637               | 1695               | 1942               | 2346               | 2424               | 2710               | 2710               | 2757               | 3859               | 5909               | 10771              | 20974              |
| *<br>Query<br>Match           | 100.0                                    | 72.0                                     | 71.6               | 71.6               | 71.2              | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               | 71.2               |
| Score                         | 50<br>36                                 | 36<br>35.8                               | 35.8               | 35.8               | 35.6              | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               | 35.6               |
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Primers AAV62497 and AAV62498 were used for the construction of the plasmid p2ZOp3J-3. The invention provides a new shuttle vector for transforming insect cells that comprises: (i) prokaryotic origin of replication; (ii) insect promoter having homology to, and capable of functioning as, an immediate early baculovirus promoter; (iii)

Disclosure; Page 39; 121pp; English.

| Aaf55402 Sequence Aaf18713 Plasmid p Aat01221 Olisgonucl Aav62171 HSV-2 Btr Abv36253 Human pro Aak85622 Human imm Abv45247 Human pro Aak85612 Human imm Aak80169 Human dig Aak89383 Human dig Aak89381 Human dig Aak89381 Human dig Aak89381 Human imm Aak85615 Human imm Aak85615 Human imm Aak85615 Human imm Aak85615 Human imm Aak85628 Human imm Aak85628 Human imm Aak85628 Human imm Aak85628 Human imm Aak8563 Human imm Aak8563 Human imm Aak85628 Human imm Aak8563 Human imm Aak8563 Human imm | Aak7346 Human imm<br>Aak69739 Human imm<br>Aak69742 Human imm<br>Aak85617 Human imm<br>Aak85618 Human imm |
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| AAF55402 AAF55403 ADL18113 AAT01221 AAV62171 AAV62171 AAV85623 AAK85619 AAK85619 AAK85615 AAK85615 AAK85615 AAK85615 AAK85623 AAK85623 AAK85623 AAK85623 AAK85623 AAK85623 AAK85623 AAK85623 AAK85623   | AAK73946<br>AAK69739<br>AAK69742<br>AAK85617<br>AAK85618  |
| 4410004014444444444   | 44444   |
| 66<br>111<br>11184<br>1173<br>1173<br>1173<br>1173<br>1173<br>1173<br>1173<br>117   | 195<br>195<br>195<br>195  |
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## ALIGNMENTS

Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins. Op ie2; promoter; shuttle vector; transformation; melanotransferrin; immediate early baculovirus promoter; prokaryotic; transcription; bleomycin/phleomycin-type antibiotic; insect cell; transposon; ion transport peptide hormone; PCR primer; ss. Hegedus DD; Pfeifer TA, Plasmid p2ZOp2J-3 constructing primer 2. Theilmann DA, BP (UYBR-) UNIV BRITISH COLUMBIA. 97US-0049946P. 98WO-CA000282. AAV62498 standard; DNA; 50 (first entry) WPI; 1998-557129/47. Grigliatti TA, WO9844141-A2 27-MAR-1997; 26-MAR-1998; 28-JAN-1998; 19-JAN-1999 08-OCT-1998 Synthetic. AAV62498; RESULT 1 AAV62498 

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          conferring resistance to a bloomycin/phleomycin-type antibiotic under transcriptional control of (ii) and (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, is useful to allow study of gene expression and direct expression of heterologous products, such as commercially important proteins. They are especially useful to allow expression of melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell in insect cells. They enable screening of lines for optimum post-translational modification of
                                                                                                                                                                                  particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                   protein expression and facilitate selection of desired transformants
prokaryotic promoter sequence, and (iv) selectable marker capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                   1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                  1 ACTIAAGCTIATAGCGATGACTGCCCGCTITCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                Length 50;
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                Sequence 50 BP; 11 A; 14 C; 12 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #25782.
                                                                                                                                                                                                                                                                                100.0%; Score 50; DB 2; L 100.0%; Pred. No. 2.4e-11;
                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS89978 standard; cDNA; 16091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                 50; Conservative
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                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS89978;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridastion probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is

Claim 1; SEQ ID NO 25782; 103pp; English.

useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food

activity of useful for g

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supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                          Sequence 16091 BP; 4724 A; 3867 C; 3861 G; 3639 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                   Length 16091;
                                                                                                                                                                                                                                                                                                                                                                                                                          8080 GITIATIGCAAICATIGCCCGCTITCCAGICGGGAAACCIGICG 8037
                                                                                                                                                                                                                                                                                             72.0%; Score 36; DB 5; Length 16v
88.6%; Pred. No. 0.00011;
....marches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #28400.
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                                                                                                                                                                                                              electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS92596 standard; cDNA; 20795 BP
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.6
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                     Query Match
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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
involving aberrant protein expression or biological activity. The bolypeptide and polymorlocide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                       Sequence 20795 BP; 4255 A; 5208 C; 5716 G; 5614 T; 0 U; 2 Other;
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72.0%; Score 36; DB 5; Length 20795; 88.6%; Pred. No. 0.00011;
                            5; Indels
                            0; Mismatches
           Local Similarity 88.6
Les 39, Conservative
 Query Match
                            Matches
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# 12363 GTTTATTGCAATCATTGCCCGCTTTCCAGTCGGGAAACCTGTCG 12406 20 7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG

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AAA87692 standard; cDNA; 745 BP 04-DEC-2000 (first entry) AAA87692; RESULT 4 AAA87692/c

Human secreted protein gene 27 SEQ ID NO:37.

Human; secreted protein; immunosuppressive; immunostimulant; nootropic; antiinfammatory; cardiant; vulnetary; antiuloer; anticonvulsant; antiparkinsonian; neuroprotective; antivoral; antibacterial; cytostatic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; cancer; immune system disorder; hyperproliferative disorder; infection; cardiovascular disorder; neurological disease; wound healing; ss. 

Homo sapiens

WO200043495-A2

27-JUL-2000

18-JAN-2000; 2000WO-US000903

99US-0116330P 19-JAN-1999; (HUMA-) HUMAN GENOME SCI INC

Moore PA; ۵, Ŋ Young PE, Ebner R, CE; Ruben SM, G, Birse Komatsoulis G, Rosen CA,

2000-499225/44. P-PSDB; AAB25691. New isolated polynucleotide encoding a secreted protein useful for preventing, treating or ameliorating a medical condition.

Claim 1; Page 394; 451pp; English.

The polynucleotide sequences given in AAA87666 to AAA87708 encodes the human secreted proteins given in AAB25665 to AAB25755. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; immunostimulant; antiinflammatory; cardiant; vulnerary; antilucer; nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective; antibacterial; anticonvulsant; antiparkinsonian; neuroprotective; antiarteriosclerotic and cytostatic. The secreted proteins and their polynucleotides can be used in gene therapy and as vaccines, chemotaxismodulators and angiogenesis-modulators. The human secreted proteins and

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                                                                                                                                            infection. AAA87657 to AAA87665 and AAB25664 represent sequences
polynucleotides can be used for diagnosing (the susceptibility to) a pathological condition by determining the presence or absence of a mutation in the polynucleotide or determining the presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer, diseases of the immune system, hyperproliferative disorders, cardiovascular disorders and neurological disease. They can also be used to promote wound healing and
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Pred. No. 6e-05;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                             168 ITAATNGCGFTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 121
                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                        Score 35.8; DB 3; Length 745; Pred. No. 5.9e-05; 0; Mismatches 8; Indels
                                                                                                                                                                                                     Sequence 745 BP; 191 A; 214 C; 188 G; 142 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 791 BP; 188 A; 198 C; 211 G; 182 T; 0 U; 12 Other;
                                                                                                                                                                                                                                                                                                                         3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site at segdata.uspto.gov/seguence.html?DocID=2003009974
                                                                                                                                                            used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breast cancer related marker, seq id 7241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 7241; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang Y, Steinmann K;
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                                                                                                                                                                                                                                          71.6%;
83.3%;
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Best Local Similarity 83.3%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN86091 standard; DNA; 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                  40; Conservative
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2004
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Purther disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN7851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence obtained after sequencing with modified Taq DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated polypeptide associated with breast cancer, useful fo detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                  Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 71.6%; Score 35.8; DB 11; Length 869; 1 Similarity 83.3%; Pred. No. 6.1e-05; 40; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 TTAATTGCGTTGCGCTNACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 616
                               544 TTAATTGCGTNGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 869 BP; 206 A; 202 C; 225 G; 216 T; 0 U; 20 Other;
           TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 4171; 36pp; English.
                                                                                                                                                           Breast cancer related marker, seq id 4171
                                                                                                                                                                                                                                                                                                                                            Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF55360 standard; DNA; 327 BP
                                                                                         ВP
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                                                                                                                                                                                                                                                                                                 18-JUL-2001; 2001US-0306220P.
                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                         ACN83021 standard; DNA; 869
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                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-787014/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             Χυ Υ,
                                                                                                                                                                                                                               US2003099974-A1.
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                                                                                                                                     02-DEC-2004
                                                                                                                                                                                                                                                     29-MAY-2003
                                                                                                                                                                                                                                                                                                                                            Lillie J,
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                                                                                                                ACN83021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF55360;
                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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net positive or net negative charge during sequencing. The recombinant thermostable DNA polymerases are useful in many recombinant DNA techniques, e.g. nucleic acid amplification by polymerase chain reaction, self-sustained sequence replication, or high temperature DNA sequencing. The recombinant thermostable DNA polymerases are also useful in increasing the uniformity of dye-terminator incorporation in fluorescent dye DNA sequencing. The present sequence represents a sequence obtained after sequencing with a modified Tag DNA polymerase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerases having an amino acid substitution at E681. The new DNA bolymerases have improved discrimination properties (and thus resulting in improved signal uniformity) and increased tolerance to high salt conditions. They also modulate the incorporation of terminators having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified recombinant thermostable DNA polymerases having amino acid substitutions at E410R or E681R, useful in recombinant DNA techniques, e.g. nucleic acid amplification or high temperature DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification describes new purified recombinant thermostable DNA
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                           chain reaction; pREFY2pref;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flicke P;
Thermostable DNA polymerase; signal uniformity; salt tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                  nucleic acid amplification; polymerase chain reaction; f
self-sustained sequence replication; DNA sequencing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 327 BP; 75 A; 82 C; 89 G; 81 T; 0.U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nampalli S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Finn PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMSH ) AMERSHAM PHARMACIA BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian cancer DNA marker #13142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 7; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nelson J, Kumar S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001WO-US009126.
                                                                                                                                                                                                                                                                                                                                10-AUG-2000; 2000WO-US022150.
                                                                                                                                                                                                                                                                                                                                                                                              99US-0150167P.
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                                                                                                                                                                                                 WO200114568-A1
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                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1999;
17-SEP-1999;
                                                                                                                               Unidentified
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The invention relates to nucleic acid markers which are overexpressed in cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the necoded by the markers, antibodies that selectively bind to the polypeptides.

CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient an antisense oligonuclecide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer sample. A difference between the marker in a patient sample and a normal level of expression of a marker in a patient sample and an ormal level of expression of a marker or sorresponds to a secreted protein or a transcribed capture corresponds to a secreted protein or a transcribed sample or its portion. The level of expression of the marker is assessed by detecting the presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein the answer is assessed by detecting the presence of a transcribed to the marker is a specifically binds with the protein or protein the answer is a seeses of by detecting the presence of a transcribed to the marker is a specifically binds with the protein or protein the marker is a specifical section of the presence of a transcribed to the marker is a specifical to the marker is a transcribed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 13142; 106pp; English.
                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                        2000US-0211940P
                                                                                      2000US-0216820P
                                                                                                              25-JUL-2000; 2000US-0220661P
21-DEC-2000; 2000US-0257672P
                                                                                                                                                                                                                                                                                                                WPI; 2001-611502/70.
                                                                                                                                                                                                                                                          Lillie J;
                                                     15-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                          Lee J,
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Gaps , **ò** 71.2%; Score 35.6; DB 5; Length 586; 82.0%; Pred. No. 6.7e-05; tive 0; Mismatches 9; Indels ( Sequence 586 BP; 168 A; 131 C; 141 G; 146 T; 0 U; 0 Other; 41; Conservative Local Similarity Query Match Matches

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516 ATTTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 565
1 ACTITAAGCTIATAGCGAIGACTGCCCGCTITCCAGTCGGGAAACCTGTCG 50
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AAS77556 standard; cDNA; 1637 BP 13-FEB-2002 (first entry) AAS77556; RESULT 

DNA encoding novel human diagnostic protein #13360.

Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.

DNA encoding novel human diagnostic protein #13349.

(first entry)

13-FEB-2002

AAS77545;

AAS77545 standard; cDNA; 1695 BP

RESULT 10 AAS77545/

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Human; chromosome mapping; gene mapping; gene therapy; forensic;
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The invention relates to isolated polynucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
cativity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
csupplement. (II) and its binding partners are useful in medical imaging
cc supplement. (II) and its binding partners are useful in medical imaging
involving aberrant protein expression or biological activity. The
polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other trails to assess biodiversity
and to produce other types of data and products dependent on DNA and
anino acid sequences. Assessed trainers the products dependent on DNA and
anino acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed encoding.
food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 13360; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                       WO200175067-A2
                                               Homo sapiens.
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WO200175067-A2

11-OCT-2001

Homo sapiens.

(HYSE-) HYSEQ INC

P-PSDB; ABG13358

biodiversity.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1183 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4942; 103pp; English.
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82.0%;
                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                         30-MAR-2001; 2001WO-US008631
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Best Local Similarity 82.0
Matches 41; Conservative
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                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                   11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid sequences. AAS94197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.2%; Score 35.6; DB 5; Length 1695; 82.0%; Pred. No. 8.8e-05; cive 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1695 BP; 415 A; 463 C; 426 G; 390 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #4942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ. ID NO 13349; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                             Tang YT;
                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity 82.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
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Gaps

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WO200175067-A2

Homo sapiens

13-FEB-2002

XSXXXXXXXXXXXXXX

AAS69138;

RESULT 11 AAS69138/c

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recardion (PCR) primers, ollowers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites captered betwee applications in disorders of sites foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and conding sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences. Absention, Note: The sequence data for this electronic format directly from WIPO at the vivolint was obtained in electronic format directly from WIPO at the vivolint was obtained in electronic format directly from WIPO at the vivolint was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.6; DB 5; Length 2424; Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2424 BP; 528 A; 721 C; 738 G; 437 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 23327; 103pp; English.
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82.0%;
   30-MAR-2001; 2001WO-US008631.
                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002 (first entry)
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                                                                                                                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                WPI; 2001-639362/73
                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                              P-PSDB; ABG23336
                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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AAS77561/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ношо
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   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in diagnostics as expressed sequence the providentifying expressed activity of (II) or to treat disease states involving (II). (II) is useful in or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polymuclocitide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and and anino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. You sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used
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                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1672 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2346 BP; 542 A; 590 C; 609 G; 605 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #23327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.6; DB 5;
Pred. No. 9.6e-05;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 13351; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                      30-MAR-2001; 2001WO-US008631
                                                                                                               2000US-00540217
2000US-00649167
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82.0%;
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Best Local Similarity 82.0
Local 41; Conservative
                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73.
P-PSDB; ABG13360.
                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                    HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity.
                                                                                                                  31-MAR-2000;
23-AUG-2000;
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11-OCT-2001
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, ss.
                             1365 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1316
1 ACTIMAGCTIATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
                                                                                                                                                                                              DNA encoding novel human diagnostic protein #13365.
                                                                                                       AAS77561 standard; cDNA; 2710 BP
                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631
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RESULT 13

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11-OCT-2001

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1080 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed carrivity of (II) is useful in gene therapy techniques to restore normal carrivity of (II) to to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for senerating and its binding partners are useful in medical imaging consupplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in calculations, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cannot acquences of the invention. Note: The sequence data for this calculation for mit or the printed specification, but was obtained in electronic format, directly from NIPO at
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chromosome marker; genetic disorder; contig; ds.
                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1080 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2710 BP; 615 A; 724 C; 690 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel DNA-related contig nucleotide sequence #455.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 13365; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE09733 standard; DNA; 2710 BP
                                                                                                                                Tang YT;
31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                2001-639362/73
                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 41; Conserv
                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                        P-PSDB; ABG13374
                                                                                                                                                                                                                                                                                                                                   biodiversity.
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ADE09733/c
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10-DEC-2002; 2002WO-US039555. 10-DEC-2001; 2001US-0339739P. 11-DEC-2001; 2001US-0339453P.

WO2003054152-A2.

REXEXEXEXEXEXEXE

03-JUL-2003.

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Gaps

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Indels

6

71.2%; Score 35.6; DB 10 82.0%; Pred. No. 9.9e-05; rative 0; Mismatches 9

41; Conservative

1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG

DB 10; Length 2710;

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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to genetic disorders. The present DNA sequences in patients to identify potential exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        analysis, characterization or therapeutic use, or as markers for tissues
in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                          Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides, useful for expressing recombinant proteins for
                                                                                                                                                                                                                                                          Zhao QA,
                                                                                                                                                                                                                                                       Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2710 BP; 615 A; 724 C; 690 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                                                                                Ren F, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 2277; 1177pp; English
                                                                                                                                                                                                                                                                               Weng G, Zh
Boyle BJ;
                                                                                                                                                                                                                                                          Goodrich RW,
                                                                                                                                                                                                                                                     Tang YT, Asundi V, Goodrich R
Ghosh M, Xue AJ, Wehrman T,
Ma Y, Wang D, Chen R, Xu C,
; 2002US-0365091P.
; 2002US-0365384P.
; 2002US-0372381P.
; 2002US-0372615P.
; 2002US-00128558.
                                                                                                                                            24-APR-2002; 2002US-0376045P
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-569235/53.
                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                             12-APR-2002;
                             14-MAR-2002;
                                                                                    12-APR-2002;
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Ma Y, Wa
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7, Appli 3, Appli 16, Appl 11, Appl 11, Appl 6, Appli 19, Appl 14, Appl 25, Appl 25, Appli 8, Appli

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

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3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
     US-09-736-457-639
US-09-614-1248-639
US-09-614-1248-639
US-09-581-184-639
US-09-58-8184-7
US-09-334-818A-7
US-09-334-818A-16
US-09-334-818A-16
US-09-334-818A-16
US-09-334-818A-18
US-09-334-818A-18
US-09-334-818A-19
US-09-334-818A-19
US-09-334-818A-19
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US-09-334-818A-19
US-09-334-818A-19
US-09-334-818A-15
US-09-334-818A-15
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Best Local Similarity 83.33
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 114, Appl
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                                                                            (without alignments)
4921.273 Million cell updates/sec
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Sequence
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                                                                  May 10, 2005, 04:19:16; Search time 16.6245 Seconds
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/bcTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-768-550-11
US-08-768-550-10
                                                                                                                                                                              1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             nucleic search, using sw model
                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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50
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                          Title:
Perfect score:
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                                                                                                               VESULE 1.

VERNATION: B4913.

APPLICANT: Kacian et al.

TITLE OF INVENTION: Highly-Purified Recombinant

TITLE OF INVENTION: Highly-Purified Recombinant

TITLE OF INVENTION: Heghly-Purified Recombinant

TITLE OF INVENTION: Heghly-Purified Recombinant

TITLE OF INVENTION: Heghly-Purified Recombinant

TITLE OF INVENTION: Highly-Purified Recombinant

TITLE OF INVENTION: Highly-Purified Recombinant

TITLE OF INVENTION: Highly-Purified Recombinant

TITLE OF INVENTION GENESS:

ADDRESSE: Gen-Probe Incorporated

STREET: 10110 Genetic Center Drive

CITY: San Diego

STREET: California

COUNTRY: USA

ZIP: 92121-4362

COMPUTER: READMAILE FORM:

MEDIUM TYPE: 3.5" Diekette, 1.44 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: Microsoft MS-DOS (Version 6.0)

SOFTWARE: RASTERO

CURRENT APPLICATION NUMBER: US/08/778,217

FILING DATE: ADBRESS

TITLE OF INVENTION NUMBER: US/08/778,217

FILING DATE: ADBRESS

TITLE OF INVENTION NUMBER: US/08/778,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,804
APPRING DATE: April 1, 1994
ATTORNEY/AGRAT INFORMATION:
NAME: Christine A. Gritzmacher
REGISTRATION NUMBER: 40,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.4%; Score 35.2; DB 2;
83.3%; Pred. No. 9.6e-06;
tive 0; Mismatches 8;
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MOLZA-A01F01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 410-8926
TELEFAX: (619) 410-8928
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 83.3%;
Matches 40; Conservative C
                                                                                                                                                                                                      LENGTH: 114
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 118 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-276-852-41/c
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Batent NO. 6593120

Batent NO. 6593120

Batent NO. 6593120

Batent NO. 6593120

BAPLICANT: RIGGS, Michael G.

APPLICANT: SORENSEN, Matthew

TITLE OF INVENTION: RECOMBINANT DNA ENCODING REVERSE TRANSCRIPTASE DERIVED FROM TITLE OF INVENTION: MOLONEY MURINE LEUKEMIA VIRUS

FILE REFERENCE: GP059-05.CP1

CURRENT APPLICATION NUMBER: US/09/397,955C

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 08/821,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/821,948
FILING DATE:

MIND DATE: March 22, 1997
CLASSIFFCATION DATA:

PRIOR APPLICATION NUMBER: 08/43,781

FILING DATE: April 1, 1994

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 40,627

REFERENCE/DOCKET NUMBER: MOLZA (New Ref.: GP059-04.FW2)

TELEPHONE: (619) 410-8926

TELEPHONE: (619) 410-8926

TELEPHONE: (619) 410-8926

TELEPHONE: (619) 410-8926

TELEPHONE: CHARACTERISTICS:
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63 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 16
                                                                                                                                                 | Sequence 1, Application US/08821948 |
| Patent No. 5998195 |
| GENERAL INFORMATION: APPLICANT: Kacion et al. |
| TITLE OF INVENTION: Highly-Purified Recombinant TITLE OF INVENTION: Reverse Transcriptase |
| NUMBER OF SEQUENCES: 13 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Gen-Probe Incorporated |
| STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92121-4362
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 18M compatible
OPERATING SYSTEM: Microsoft MS-DOS (Version 6.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Best Local Similarity 83.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-397-955C-1/c
                                                                                                                                         US-08-821-948-1/c
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Gaps
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide used to construct plasmid pUC 18N
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Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Butcon, Dennis R
APPLICANT: Barbes, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.2; DB 5; Length 118; Pred. No. 9.7e-06; Mismatches 8; Indels (
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70.4%; Score 35.2; DB 4; Length 114;
Best Local Similarity 83.3%; Pred. No. 9.6e-06;
Matches 40; Conservative 0; Mismatches 8; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HIGHLY-PURIFIED RECOMBINANT REVERSE TITLE OF INVENTION: TRANSCRIPTASE NUMBER OF SEQUENCES: 18
NUMBER OF SEQUENCES: 18
NUMBER OF SEQUENCES: 18
COMPUTER READABLE FORM:
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04092
PRIOR APPLICATION NUMBER: 08/443,781
PRIOR FILING DATE: 1995-05-18
PRIOR APPLICATION NUMBER: 08/221,804
PRIOR FILING DATE: 1994-04-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 1
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; GENERAL INFORMATION:
; APPLICANT:
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Patent No. 5759817
GENERAL INFORMATION:
APPLICANT: BLADAS, Carlos
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5759817th Torrey Pines Road, Suite 220,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,730A
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.2; DB 1;
Pred. No. 1.1e-05;
0; Mismatches 8;
                                                                                                                CIALING DATE:
CIASSIFICATION: 435
CIASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
PRIOR APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTONNEY AGENT INFORMATION:
NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCRF 238.2
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10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEG ID NO: 114: SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 40; Conservative
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                                                                                            08-JUN-1994
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STREET: Mail Drop TPC8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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| Patent No. 5658727
| GENERAL INFORMATION:
| APPLICANT: Rang, Angray | APPLICANT: Barbas, Carlos | APPLICANT: Lerner, Richard A. TITLE OF INVENTION: HATERODIMERIC RECEPTOR LIBRARIES USING TITLE OF INVENTION: PHAGEMIDS | NUMBER OF SEQUENCES: 161 | CORRESPONDENCE ADDRESS: ADDRESSE: ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5552138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
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Pred. No. 1.1e-05;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                         COMPLIER REALCHELS Floppy disk
COMPUTER: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
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Best Local Similarity 83.3%;
Matches 40; Conservative
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INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid sTRANDEDNESS: double
                                                                                                                                                                                                                       ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                              La Jolla
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HYPOTHETICAL: NO
HATI-SENSE: NO
US-08-276-852-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-133-011-114/c
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                                                                                                                                                                                             COUNTRY:
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Gaps

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DNA (genomic)
NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
                                                                                                                                                                                                                                                                           40; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
   MOLECULE TYPE:
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                                                                           ; ANTI-SENSE:
US-08-387-874-87
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Patent No. 5770356

GENERAL INFORMATION:
APPLICANT: Light, Paul L., II
APPLICANT: Light, Paul L., II
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PHAGEMIDS COEXPRESSING A SURFACE
TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
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STATE: Ca
COUNTRY: USA
COMPUTER: Ea Jola
COMPUTER: En John
COMPUTER: En John
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,874
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CT/US93/08364
FILING DATE: 03-SEP-1993
PRIOR APPLICATION NUMBER: US/08/387,874
FILING DATE: 03-SEP-1993
PRIOR APPLICATION NUMBER: US/08/387,369
FILING DATE: 04-SEP-1992
ATPONEY/AGENT INFORMATION:
ANDE: Citizen Properation: Properation Pro
                                                                                                               SCR0707P
                               NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCRO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-784-9397
TELEPAX: 619-784-9399
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REGISTRATION NUMBER: 34,163
REFRENCE/DOCKET NUMBER: TSR1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-6312
                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 114: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic); HYPOTHETICAL: NO .; ANTI-SENSE: NO .; US-08-322-730A-114
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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nucleic acid
EDNESS: double
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                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Barton, Dennis R
APPLICANT: Barton, Carlos F
APPLICANT: Barton, Carlos F
APPLICANT: Barton, Carlos F
APPLICANT: Barton, Carlos A
TITLE OF INVENTION: HUMAN INFORMALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pacent Counsel
ADDRESSEE: Pacent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
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Score 35.2; DB 1; Length 201; Pred. No. 1.1e-05;
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                                                                                                                                                                         65 rizarrecerrecercacrececerriceaerceeaaacereire 18
                                                                                                                    3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                             8; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION NUMBER: US/08/899,575
PILING APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
FILING APPLICATION DATA:
APPLICATION DATE: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                          0; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/08899575 Patent No. 5770440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
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     Query Match 70.4%;
Best Local Similarity 83.3%;
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FILING DATE:
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US-08-383-619-114
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APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
FILING DATE: 30-SEP-1993
FILING DATE: 30-SEP-1993
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTONNEY/AGENT INPORMATION:
NAME: APPLICATION THOMSA
                                               65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REPERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2337
TELEPHAX: 619-554-6312
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; Sequence 114, Application US/08383619
; Patent No. 5955341
                                                                                                                                                                       Sequence 41, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-08-899-575-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL: 1
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A WARLLANT: BEATHER, RICHARD

A PRICIARY: LEATHER RICHARD

ITLE OF INVENTIOR: HERRENDUMENT EXCEPTOR LIBRAHES USING

ITLE OF INVENTIOR: HERRENDUMENT EXCEPTOR LIBRAHES USING

ITLE OF INVENTIOR: HERRENDUMENT EXCEPTOR LIBRAHES USING

CORRESS: DOUGLAN & BUNGARM

ADDRESSE: DOUGLAN & BUNGARM

CORRESS: DOUGLAN & BUNGARM

APPLICATION NUMBER: US/08/381,619

FILLING DATE: DATE

FILLING DATE: DATE

ATTORNALISMS: DATE

FILLING DATE: BUNGARM: US/08/381,619

FILLING DATE: BUNGARM: US/08/381,619

FILLING DATE: BUNGARM: US/08/381,619

ATTORNALISMS: DATE

FILLING DATE: BUNGARM: US/08/381,619

FILLING DATE: BUNGARM: US/08/381,719

BERT LOCAL SIMILARITY BUNGARM: US/08/381,719

BERT LOCAL SIMILARIT
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TITLE OF INVENTION: PHAGEMIDS COEXPRESSING A SURFACE
TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
NUMBER OF SEQUENCES: 97
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US7/941,369
FILING DATE: 04-SEP-1992
INFORMATION FOR SEQ ID NO: 87:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.2; DB 3;
Pred. No. 1.1e-05;
0; Mismatches 8;
                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET WUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                           APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-348-1992
FILING DATE: 27-348-1992
FILING DATE: 17-348-1992
FILING DATE: 10-348-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                          08/133,011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 87, Application PC/TUS9308364 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                  TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TTAAGCTTATAGCGATGACTG
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative
    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 83.3
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
PCT-US93-08364-87/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-729-597-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
PCT-US93-08364-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8 STREE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 70.4%; Score 35.2; DB 3; Length 201; 1 Similarity 83.3%; Pred. No. 1.1e-05; 40; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TIMAGCTIATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,597
FILING DATE: 04-Dcc-2000
CLASSIFICATION: 435
                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,739
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION UNDRER: PCT/US 92/03091
FILING DATE: 10-APP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 114, Application US/09729597
Patent No. 6468738
GENERAL INFORMATION:
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,011
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kang, Angray
Barbas, Carlos
Lerner, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHAGEMIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFRENCE/DOCKET NUMBER: SCRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-557 7. 1 INFORMATION FOR SEQ ID NO: 111 SEQUENCE CHARACTERISTICS: 1 LENGTH: 201 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92037
COMPUTER READABLE FORM:
                                             COMPUTER: IBM PC
OPERATING SYSTEM:
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Matches 40; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO US-08-907-739-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-729-597-114/c
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Gaps

Gaps

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Query Match 70.4%; Score 35.2; DB 5; Length 201; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8; Indels C
                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                           PCT-US95-08743-41
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65 TTAATTGCGTTGCGCTCACTGCCCCTTTCCAGTCGGGAAACCTGTCG 18 3 TTAAGCTTATAGCGATGACTGCCCGCT

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Gaps

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Search completed: May 10, 2005, 07:29:36 Job time : 17.6245 secs

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May 10, 2005, 05:52:55 ; Search time 141.277 Seconds (without alignments) 2164.037 Million cell updates/sec
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/cgni_6/prodata///pubpna/USOP_NEW_PUB.seq:*
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*

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5: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

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8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5654200 seqs, 3057283753 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                       US-09-896-888A-10
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    |           |             |                     |                   |                    |                    |                     | ٠                   |                    |                    |                    |                    |                     |
|----|-----------|-------------|---------------------|-------------------|--------------------|--------------------|---------------------|---------------------|--------------------|--------------------|--------------------|--------------------|---------------------|
|    | 1000      | Describeron | Sequence 10, Appl   | Sequence 37, Appl | Sequence 7241, Ap  | Sequence 4171, Ap  | Sequence 80752, A   | Sequence 13142, A   | Sequence 2086, Ap  | Sequence 2087, Ap  | Sequence 2086, Ap  | Sequence 2087, Ap  | Sequence 88806, A   |
|    | Ç.        | ar ar       | 9 US-09-896-888A-10 | US-09-985-153-37  | US-10-198-846-7241 | US-10-198-846-4171 | US-10-437-963-80752 | US-09-814-353-13142 | US-10-027-632-2086 | US-10-027-632-2087 | US-10-027-632-2086 | US-10-027-632-2087 | US-10-437-963-88806 |
|    | 9         | 9           | 6                   | 11                | 14                 | 14                 | 18                  | 10                  | 13                 | 13                 | 11                 | 17                 | 18                  |
|    | 1000      | nengen      | 20                  | 745               | 791                | 869                | 415                 | 586                 | 865                | 865                | 865                | 865                | 2307                |
| dР | Query     | FIACCI      | 100.0               | 71.6              | 71.6               | 71.6               | 71.2                | 71.2                | 71.2               | 71.2               | 71.2               | 71.2               | 71.2                |
|    | 3         | 200         | 20                  | 35.8              | 35.8               | 35.8               | 35.6                | 35.6                | 35.6               | 35.6               | 35.6               | 35.6               | 35.6                |
|    | ult<br>No |             | -                   | 7                 | m                  | 4                  | ហ                   | ø                   | 7                  | 80                 | 0                  | 10                 | 11                  |
|    | Result    | į           |                     | υ                 |                    |                    | U                   |                     | U                  | U                  | U                  | υ                  | υ                   |
|    |           |             |                     |                   |                    |                    |                     |                     |                    |                    |                    |                    |                     |

RESULT 2

| 2259, A 2266, A 400   | ٥  |
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| 864477988941807   | Gaps   |
| Sequence Seq  | 50 50  |
| Sequence Seq  | Primer<br>50;<br>18<br>TGTCG<br>TGTCG  |
|   | nce: Fength Indel  |
| 6625<br>6625<br>6727<br>6727<br>6727<br>6737<br>6737<br>674<br>674<br>674<br>674<br>674<br>674<br>674<br>67   | Sequence: 9, Lengt 0, Ind TCGGGAAAC  |
| 10-437-963-392 10-357-930-452 10-357-930-452 10-357-930-452 10-764-846-347 10-091-483-341 10-091-483-341 10-016-986-41 10-016-986-41 10-018-986-41 10-018-986-41 10-018-986-41 10-018-986-41 10-018-986-41 10-018-986-41 10-018-986-41 10-018-986-41 10-018-986-41 10-018-986-688-15 10-018-988-15 10-018-988-15 10-018-988-17 10-018-988-17 10-018-988-17 10-018-988-17 10-018-988-17 10-018-018-018-018 10-018-018-018-018-018 10-018-018-018-018-018-018-018-018-018-0   | cial paragraph of the corrected of the c |
| 10.437-963<br>-10.437-963<br>-10.357-930<br>-10.357-930<br>-10.764-891<br>-10.001-4891<br>-10.001-986<br>-10.001-986<br>-10.001-986<br>-10.357-930<br>-10.357-930<br>-10.357-930<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-549<br>-10.286-17-963<br>-10.165-856<br>-10.165-856<br>-10.165-856<br>-10.165-856<br>-10.165-856<br>-10.165-856<br>-10.165-856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-8856<br>-10.165-88   | Artificial ore 50; DB ed. No. 1.8 Mismatches CCCGCTTTCCA   |
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| 10. Appl. 10  | DISSONA<br>SM: Artific<br>EE:<br>EB:<br>BBBA-10<br>CCh<br>al Similari<br>SO; Cons<br>1 ACTTAAG   |
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CURRENT APPLICATION NUMBER: US/10/198,846

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; LOCATION: 282, 300, 554, 592, 650, 707, 720, 728, 755, 767, 775, 791
; CTHER INFORMATION: n = A.T.C or G
US-10-199-846-7241
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                                                                                                                                                                                                                                                                                                                                                                                       Length 791;
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APPLICANT: Millie, James
APPLICANT: Wangy o
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APPLICANT: Wangy o
APPLICANT: Wangy o
APPLICANT: Wangy Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, K.
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MKI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 00/2-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7241
LENGTH: 791
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4171
LENCTH: 869
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; LOCATION: 2, 3, 4, 6, 9, 10, 11, 531, 5;
; LOCATION: 763, 764, 780, 816, 841, 856
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-4171
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; Sequence 80752, Application US/10437963
; Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4171, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFERENCE: PZ036P1
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/985,153
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/618,150
PRIOR FILING DATE: 2000-07-17
PRIOR PELICATION NUMBER: PCT/US00/00903
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 1999-01-19
PRIOR PILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.0
LENGTH: 745
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Publication No. US20030099974A1
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
Sequence 37, Application US/09985153 Publication No. US20040181047A1 GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: (727)
OTHER INFORMATION:
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

FEATURE:

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
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                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 231
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                                                                                                                                                                              FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 2086
LENGTH: 865
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Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . NAME/KEY: misc_feature
i LOCATION: (1)...(865)
c OTHER INFORMATION: n = A,T,C or G
US-10-027-622-2086
      US20020198371A1
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ORGANISM: Human
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                                                                                            APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 80752
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APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-OGES
CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: US 60/191,031
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PELING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PLING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
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Pred. No. 4.4e-05;
0; Mismatches 9; Indels 0
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Pred. No. 4.6e-05;
0; Mismatches 9;
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US-10-437-963-80752
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030165831A1
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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82.0%;
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Best Local Similarity 82.0%;
Matches 41; Conservative
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Best Local Similarity 82.0°
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Oryza sativa
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US-09-814-353-13142
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US-10-027-632-2086/c
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Sequence 2086, Application US/10027632

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RESULT 12
US-10-437-963-39259/c
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/18,006
PRIOR PELIOR APPLICATION NUMBER: US 60/18,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR PELIOR NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastESEQ for Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                           Query Match 71.2%; Score 35.6; DB 13; Length 865; Best Local Similarity 82.0%; Pred. No. 5e-05; Matches 41; Conservative 0; Mismatches 9; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2086, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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US-10-027-632-2086
                                                                                 LOCATION: (1) ... (865)
, OTHER INFORMATION: n = A,T,C or G
US-10-027-632-2087
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                                                    NAME/KEY: misc feature
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US-10-027-632-2087/c
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.2%; Score 35.6; DB 17; Length 865; 82.0%; Pred. No. 5e-05; tive 0; Mismatches 9; Indels 0.
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6e-05;
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US-10-437-963-88806
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82.0%; Pred. No. 6e-0
ive 0; Mismatches
            PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-18
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
SOFTWARE: FASESO for Windows Version 4.0
SEQ ID NO 2087
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APPLICATION NUMBER: US 60/218,006
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    LOCATION: (1)...(865)
    OTHER INFORMATION: n = A,T,C or G
US-10-027-632-2087

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Best Local Similarity 82.0%
Matches 41; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-437-963-88806/c
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
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APPLICANT: SCRIEGE. KOUSEL
APPLICANT: Bridge, Wilson
APPLICANT: Bridge, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: WINBER: 09/785,276
PRIOR PELICATION NUMBER: 09/785,276
PRIOR PELICATION NUMBER: 09/785,276
PRIOR PELICATION NUMBER: 60/113,319
PRIOR PELICATION NUMBER: 60/13,319
PRIOR PELICATION NUMBER: 60/207,454
PRIOR PELICATION NUMBER: 60/207,454
PRIOR PELICATION NUMBER: 60/211,314
PRIOR PELICATION NUMBER: 60/211,314
PRIOR PELICATION NUMBER: 60/219,007
PRIOR PELICATION NUMBER: 60/219,007
PRIOR PELICATION NUMBER: 60/219,007
PRIOR PELICATION NUMBER: 60/219,007
PRIOR PELICATION NUMBER: 60/219
PRIOR PELICATION NUMBER: 60/219
PRIOR PELING DATE: 2000-06-09
PRIOR PELING DATE: 2000-01-18
PRIOR PELING DATE: 2000-01-18
PRIOR PELING DATE: 2000-01-213
NUMBER: OF SEQ ID NOS: 62232
SOFTWARE: FRANCESCE FOR WINGOWS VETBION 4.0
SEQ ID NO 45266
LENGTH: 1199
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                                                                                              63 rraarrgcgrrgcgcrcacrgcccccrrrccagrcggaaaccrgrcg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGAAACCTGTCG 115
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 347
LENGTH: 195
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                                          3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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Patent No. US20020102638A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT APPLICATION WURBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
LOCATION: (159)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: SITE
                                                                                                                                                                                                                                     Sequence 45266, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schlegel. Robert
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 40; Conserv
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US-10-357-930-45266
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US-09-764-846-347
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                                                                                                                                                                                                                                                                                        APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SCALEGE: Wilson
APPLICANT: SCALEGE: Wilson
APPLICANT: SCALEGE: Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE
CURRENT APPLICATION NUMBER: 05/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-06-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 62232
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PASELSEQ FOR WINDOWN VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACTIAAGCTIAIAGCGAIGACIGCCCGCTITCCAGICGGGAAACCIGICG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AATCATGGTCATAGCTGTTTCTGCCCGCTTTCCAGTCGGGAAACCTGTCG 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_42817C.1
US-10-437-963-39259
Sequence 39259, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wo, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36271, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
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Best Local Similarity
Matches 40; Conserval
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LENGTH: 2721
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LENGTH: 173
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Gaps Ouery Match
70.4%; Score 35.2; DB 9; Length 195;
Best Local Similarity 83.3%; Pred. No. 5.6e-05;
Matches 40; Conservative 0; Mismatches 8; Indels 0 LOCATION: (164)
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NAME/KEX: SITE
LOCATION: (166)
COTHER INFORMATION: n equals a,t,g, or c
LOCATION: (193)
COCATION: (193)
COTHER INFORMATION: n equals a,t,g, or c
US-09-764-846-347 g ð

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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                    Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description   | Sequence 10. Appl | edilence 10.   | -             | 257              | 284            | 37,      | 37        | equence 37 | 86            | 8            | 72              | e<br>4           | ည်း<br>မ         | e 1314            | 13142,          |                  | 2087             | 2086         | 2087       | 1974,           | e 1974     | 13360       | σ          | 4942,           | e 8880      | 13351       | 23327      | 13365    | , 2277,     | e 3925      | e 5677,    | e 5236,    | a)         | e 2281,         | e          | edneuce      | O)        | 9           | equence | equence           | quence       | ce 200,   | Sequence 200, App | Sequence 36271, A    | equence 3627    |
|-----------|---------------|-------------------|----------------|---------------|------------------|----------------|----------|-----------|------------|---------------|--------------|-----------------|------------------|------------------|-------------------|-----------------|------------------|------------------|--------------|------------|-----------------|------------|-------------|------------|-----------------|-------------|-------------|------------|----------|-------------|-------------|------------|------------|------------|-----------------|------------|--------------|-----------|-------------|---------|-------------------|--------------|-----------|-------------------|----------------------|-----------------|
| SUMMERTES | ID            | US-09-048-911-10  | S-09-896-888-1 | -09-896-888A- | -US01-08631-2578 | -US01-08631-28 | -00903-3 | -618-150- | 5-153-3    | -10-100-683-9 | -11-001-793- | -10-198-846-724 | -10-198-846-4171 | S-10-437-963-807 | -09-814-353-1314Z | -09-814-353A-13 | -09-634-306B-208 | -09-634-306B-208 | -027-632-208 | 27-632-208 | -US01-08656-197 | 73-573-197 | -08631-1336 | -08631-133 | -US01-08631-494 | 37-963-8880 | -08631-1335 | 08631-2332 | 31 - 133 | .39555A-227 | 37-963-3925 | -08631-567 | -08631-523 | -08631-217 | -US01-14827-228 | 77-408-321 | r-us01-08631 | 38-221-80 | -08-443-781 | -293A-5 | US-09-426-293B-52 | 08-123-456-2 | -09-297-4 | -09-994-404-20    | US-09-785-276A-36271 | -10-357-930-362 |
|           | DB            |                   |                | 38            | -                | -              | Н        | 27        |            |               | 68           | 49              | 49               |                  |                   | 32              |                  |                  | 4            | 46         |                 |            |             | н          |                 | -           | -           |            | •        |             |             |            | 7          |            | П               |            | 7            | ۵         | 10          | 22      | 22                | 7            | 19        |                   | 34                   |                 |
|           | Length        | 50                | 50             | 20            | 609              | 20795          | 4        | 4         | 4          | 4             | 745          | σ               | 869              | - 0              | n a               | 9               | 865              | 865              | 865          | 865        | 666             | 666        | 1637        | 1695       | 1942            | 2307        | 2346        | 2424       | 2710     | 2710        | 2721        | 2757       | S          | 0          | 9               | 16122      | 097          | 118       | н           | m       | 134               | 151          |           | 151               | 173                  | 173             |
| ٠.        | ery           | 0.00              |                |               | 72.0             | ď              | ä        | ä         | 71.6       | ä             | 71.6         | ä               | 71.6             |                  | ٠                 | •               | 71.7             |                  | 71.2         |            | ٠               | ٠:         |             | ٠          | 71.2            | ٠           | •           | •          | 71.2     | •           | •           | •          |            | •          |                 | ä          | 1.2          | 4.0       | 70.4        | 4.0     | 4.0               | 4.0          | 4.0       |                   |                      | 4.0             |
| •         |               | !                 |                | 100           |                  |                |          |           |            |               |              |                 |                  |                  |                   |                 |                  |                  |              |            |                 |            |             |            |                 |             |             | -1         |          |             |             | ١٠.        |            | -          |                 |            |              |           |             | 7       | 7                 | 7            | 7         |                   | 7                    |                 |
|           | Score         | 50                | 000            | 20            | 36               | 36             | 'n.      | 'n        | 'n.        | ņ.            | ŝ            | ď.              | 32.8             |                  | n 1               | 35.6            | n ı              | <br>             | Š            | 'n         | ď.              | 'n.        | 5.          | Ľ.         | 35.6            | 35.6        | 35.6        | 35.6       | 35.6     | 35.6        | 35.6        | 35.6       | 35.6       | 35.6       | ٠               | ů.         | ٠            | 2         | 'n          | 'n      | 5                 | 35.2         | 5         | •                 | 35.2                 | 35.2            |
|           | Result<br>No. | -                 | 7              | m             | Ω<br>4           | Ŋ              | 9        |           |            | 0             | _            | 11              | 12               | 5 T T            | # !<br>           | ٠,              | ٠,               | ٠,               | -1           | -          | N               | N          | ~           | c 23       | N               | N           | 56          | 0          | N        | N           | c 30        | m          | n          | r)         | 9.4             | 32         | m            | c 37      | m           | 39      | 40                | 41           | 42        | 43                | 44                   | 45              |

Gaps Gaps ö .. 0 20 20 20 1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Primer ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-896-888-10 1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1 ACTITAAGCITTAIAGCGAIGACTGCCCGCTTTCCAGICGGGAAACCTGTCG 1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG Query Match 100.0%; Score 50; DB 16; Length 50; Best Local Similarity 100.0%; Pred. No. 2.9e-10; Matches 50; Conservative 0; Mismatches 0; Indels Length 50; Indels 100.0%; Score 50; DB 38; 100.0%; Pred. No. 2.9e-10; rative 0; Mismatches 0; US-09-048-911-10

Sequence 10, Application US/09048911

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Insect Expression Vectors

TILLE REPERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/048,911

CURRENT FILING DATE: 1998-03-26

EARLIER FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 10

LENGTH: 50 APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44
FULE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US 09/048,911
PRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1997-03-27
FRIOR FILING DATE: 1997-03-27
SOFTWARE: PATENTIN NOWS: SO
SOFTWARE: PATENTIN Ver. 2.0 US-05-896-888A-10
Sequence 10, Application US/0989688BA
Sequence 10, Application US/0989688BA
GENERAL INFORMATION:
APPLICANTION:
TITLE OF INVENTION: Innect Expression Vectors
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888BA
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26 US-09-896-888-10; Sequence 10, Application US/09896888; GENERAL INFORMATION: TYPE: DNA ORGANISM: Artificial Sequence TYPE: DNA ORGANISM: Artificial Sequence FEATURE: Conservative Query Match Best Local Similarity Matches 50; Conserv US-09-048-911-10 LENGTH: RESULT 3 ò g g 8

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ALIGNMENTS

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NAME/KEY: SIMILAR

COCATION: (961).. (899)

COTHER INFORMATION: 100% homologous to Cloning vector pBACe3.6

OTHER INFORMATION: 1evansucrase, accession number U80929, Smith-Waterman Score=110.

NAME/KEY: misc_feature

LOCATION: (1)...(20795)

COTHER INFORMATION: n = a,t,c or g

PCT-US01-08631-28400
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                                                                                                                                                                                                                                                                                                                                                                                   7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
PCT-US00-00903-37/C
Sequence 37, Application PC/TUS0000903
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFERENCE: PZ036.PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/USOO/00903
CURRENT FILING DATE: 2000-01-18
EARLIER APPLICATION NUMBER: 60/116,330
EARLIER FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 745
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NAME/KEY: SITE
LOCATION: (48)
OTHER INFORMATION: n equals a,t,g, o
FEATURE:
NAME/KEY: SITE
LOCATION: (93)
OTHER INFORMATION: n equals a,t,g, (
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OTHER INFORMATION: n equals a,t,g,
PRATURE:
LOCATION: (27)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
PEATURE:
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            TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LOCATION: (739)
OTHER INFORMATION: n
FEATURE:
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OTHER INFORMATION:
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LOCATION: (745)
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NAME/KEY: SITE
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NAME/KEY:
                                                          FEATURE:
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; OTHER INFORMATION: levansucrase, accession number U80929, Smith-Waterman Score=1333.
PCT-US01-08631-25782
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                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-896-888A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; Length 16091;
Pred. No. 0.00073;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 50; DB 38; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 50; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFREENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCTUSO1-08631-28400

Sequence 28400, Application PC/TUSO108631

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REPERENCE: 21272-049

CURRENT APPLICATION NUMBER: PCT/USO1/08631

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PILING DATE: 2000-03-31

FRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEQ ID NO 28400

LENGTH: 20795
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PCT-US01-08631-25782/c
Sequence 25782, Application PC/TUS0108631
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 50
                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.6%;
Matches 39; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                               PEATURE:
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NAME/KEY:
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                                                                                                                                                        3 TTAAGCTTATAGCGATGACTGCCCCGCTTTCCAGTCGGAAACCTGTCG 50
                                                                                                                                 3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
                                                      Length 745;
                                                                                            Indels
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 33 Human Secreted Proteins TITLE OF INVENTION: 33 Human Secreted Proteins FILE REFERENCE: PO20461 FULL REFERENCE: PO20461 FULL REPERENCE: 2000-07-17 FURENT FILING DATE: 2000-07-17 PRIOR APPLICATION NUMBER: 60/116,330 PRIOR FILING DATE: 1999-01-19 FRIOR FILING DATE: 1999-01-19 FRIOR FILING DATE: 1999-01-19 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 37
                                                    Score 35.8; DB 1;
Pred. No. 0.00049;
0; Mismatches 8;
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; OTHER INFORMATION: n equals a,t,g, or c PCT-US00-00903-37
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                                                                                                                                                                                                                                                          Sequence 37, Application US/09618150
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,g,
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                                                      71.68;
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                                                                                              40; Conservative
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ORGANISM: Homo sapiens
                                                                    Best Local Similarity
Matches 40; Conserv
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LOCATION: (739)
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US-09-618-150-37/c
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                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.6%; Score 35.8; DB 45;
83.3%; Pred. No. 0.00049;
tive 0; Mismatches 8;
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFERENCE: P2036P1
CURRENT APPLICATION NUMBER: US/09/985,153
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/618,150
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR PLING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR PILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR PILING DATE: 1997-05-23
PRIOR PLING DATE: 1997-05-23
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: n equals a,t,g, or c
US-09-985-153-37
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INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
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sequence 37, Application US/09985153

RESULT 8 US-09-985-153-37/C

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CURRENT FILING DATE: 2004-12-02
PRIOR FLILING DATE: 2004-12-02
PRIOR FLILING DATE: 2004-12-02
PRIOR FLILING DATE: 2002-13-19
PRIOR FLILING DATE: 1997-03-19
PRIOR PLICATION NUMBER: US 60/040,162
PRIOR FLILING DATE: 1997-03-07
PRIOR PLILING DATE: 1997-04-11
PRIOR FLILING DATE: 1997-04-11
PRIOR FLILING DATE: 1997-04-11
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-04-11
PRIOR PLILING DATE: 1997-06-23
PRIOR PLING DATE: 1997-06-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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; COTHER INFORMATION: n equals a,t,g, or c
US-11-001-793-981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (739)..(739)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMENTER: misc feature LOCATION: (3)...(3) OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (727)..(727)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (93) ...(93)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (27) ... (27)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (163) ..(163)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc_feature
LOCATION: (48)..(48)
OTHER INFORWATION: n equals
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 13468 SOFTWARE: PatentIn Ver. 2.0
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; Sequence 981, Application US/11001793
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/043,580
PRIOR FILING DATE: 1997-04-11
PRIOR PLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR PLING DATE: 1997-08-22
PRIOR PAPLICATION NUMBER: US 60/043,314
PRIOR PLING DATE: 1997-04-11
PRIOR PLING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/043,314
PRIOR PLING DATE: 1997-05-23
PRIOR PLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR PLING DATE: 1997-05-23
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NAME/KEY: misc feature
LOCATION: (745)...(745)
OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (3). 7(3)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (48)...(48)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (163)...(163)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (27) ... (27)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (93) ... (93)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (727)..(727)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc_feature
LOCATION: (739). (739)
OTHER INFORMATION: n equals a,t,g,
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OCATION: (113)...(113)
JTHER INFORMATION: n equals a,t,g,
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LENGTH: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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; TYPE: DNA
; ORGANISM: Homo s
US-09-814-353-13142
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                                                                                                           Sequence 7241, Application US/10198846
GENERAL INFORMATION:
APPLICANT: Lille, James
APPLICANT: Lille, James
APPLICANT: Wi, Yongwan
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
ITILE OF INVENTION: THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FRACE FRACE FRACE FRACE
SEQ ID NO 7241
LENGTH: 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 282, 300, 554, 592, 650, 707, 720, 728, 755, 767, 775, 791
; CTHER INFORMATION: n = A,T,C or G
US-10-198-846-7241
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PREVENTION, AND
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; LOCATION: 2, 3, 4, 6, 9, 10, 11, 531, 585, 667, 691, 696, 732, 742,

; LOCATION: 763, 764, 780, 816, 841, 856

; OTHER INFORMATION: n = A,T,C or G
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168 rraarngcgrrdcgcrcacrcccccrrrccacrccccaaaccrcrcrc 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.6%; Score 35.8; DB 49; Length 869; 83.3%; Pred. No. 0.00051; tive 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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; GENGRAL INFORMATION:
GENGRAL INFORMATION:
APPLICANT: LINIE, James
APPLICANT: Ku, Yongyao
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: WOUBER: US/10/198,846
CURRENT APPLICATION NUMBER: US/10/198
CURRENT FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4171
LENGTH: 869
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Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                 US-10-198-846-7241
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US-10-198-846-4171
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Sequence 80752/C

Sequence 80752, Application US/10437963

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Ed. Rosa, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53221)

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 80752

LENTH: 415
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Sequence 13142, Application US/09814353

GENERAL INFORMATION:

APPLICANT: Lee, John
APPLICANT: Lilie, James

ITILE OF INVENTION: NOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

PILE REPERENCE: NAI-OGGE

CURRENT APPLICATION NUMBER: US 60/191,031

PRICH FILING DATE: 2000-03-21

PRICH FILING DATE: 2000-05-25

PRICH FILING DATE: 2000-07-07

PRICH FILING D
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Pred. No. 0.00054;
0; Mismatches 9;
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COTHER INFORMATION: Clone ID: PAT_MRT4530_80346C.1
US-10-437-963-80752
TTAAGCTTATAGCGATGACTGCCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 82.0%;
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ORGANISM: Oryza sativa
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US-09-814-353-13142
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; Sequence 13142, Application US/09814353A
; Sequence 13142, Application:
APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: WUMBER: US/09/814,353A
CURRENT FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13142
                                               Gaps
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                                                                                                                                  516 ATTTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 565
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                                                                                            1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
Score 35.6; DB 35; Length 586;
Pred. No. 0.00057;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.6; DB 35; Length 586; Pred. No. 0.00057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
Query Match
Best Local Similarity 82.0%;
Matches 41; Conservative
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Best Local Similarity 82.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-814-353A-13142
                                                                                                                                                                                                      RESULT 15
US-09-814-353A-13142
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516 ATTTAATTGCGTTGCGCTCACTGCCCCCTTTCCAGTCGGGAAACCTGTCG 565

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Search completed: May 10, 2005, 09:18:57 Job time : 414.906 secs

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Sequence 28400, A
Sequence 13360, A
Sequence 13360, A
Sequence 13351, A
Sequence 13351, A
Sequence 23327, A
Sequence 23327, A
Sequence 5236, A
Sequence 5236, A
Sequence 21710, A
Sequence 21713, A
Sequence 21713, A
Sequence 1746, Ap
Sequence 1748, Ap
                                                                                                                 May 10, 2005, 05:51:35; Search time 123.262 Seconds (without alignments) 834.449 Million cell updates/sec
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                                                                                                                                                                                                                                      1 acttaagcttatagcgatga.....tccagtcgggaaacctgtcg
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*

12: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*

12: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*

13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                            18797578
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-450-763-25782

US-10-450-763-13340

US-10-450-763-13349

US-10-450-763-13349

US-10-450-763-13349

US-10-450-763-1335

US-10-450-763-23327

US-10-450-763-2537

US-10-450-763-2537

US-10-450-763-28399

US-10-450-763-21710

US-10-450-763-21710

US-10-450-763-21710

US-10-450-763-21710

US-10-450-763-21710

US-10-450-763-21773

US-10-450-763-21773
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                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     9398789 segs, 1028555566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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16091
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                     Searched:
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US-10-450-763-10137 US-10-841-603B-20

| 544 Sequence 2544, Ap Sequence 2578, Ap Sequence 18863, A Sequence 18863, A Sequence 18863, A Sequence 55, Appl Sequence 102521, Sequence 13803, Ap Sequence 13803, Ap Sequence 54, Appli Sequence 54, Appli Sequence 54, Appli Sequence 18949, A Sequence 1156, Ap Sequence 1156, Appli Sequence 1156, Appli Sequence 1156, Appli Sequence 2551, Appli Sequence 104007, Sequence 28930, A Sequence 551, Appli Sequence 551, Ap | Other Molecules Associated With  | 8; DB 9; Length 451; .8e-06; .ches 7; Indels 0; Gaps 0; CCAGTCGGGAAACCTGTCG 50                    |
|--|--|---|
| 456 10 US-11-090-997-2544 473 8 US-11-090-997-2578 473 8 US-10-450-763-18863 508 2 PCT-US05-06626-428 519 8 US-10-450-763-18863 519 8 US-10-450-763-1893 526 2 PCT-US05-06626-54 527 10 US-10-450-763-13893 526 2 PCT-US05-06626-54 5240 11 US-11-022-1022 52 2 PCT-US05-06626-54 5240 11 US-11-022-1022 52 6 2 PCT-US05-06626-7 52 8 US-10-450-763-18949 685 13 US-60-655-875-88381 686 9 US-10-472-963-174 686 9 US-10-472-963-174 686 9 US-10-472-963-174 713 0 US-11-090-997-2551 714 0 US-11-090-997-2551 715 1 US-11-030-997-2551 716 2 US-10-472-963-174 717 8 US-10-703-032-74322 718 1 US-10-703-032-74322 719 1 US-10-703-032-144007 718 1 US-10-450-763-104007 718 1 US-10-450-763-104007 719 1 US-10-450-763-104007  | es And 2   | 3 ITT   |
| 2 2 3 3 5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6  | 1 703-032-10256 ence 102508, Encl INCOMATI LICANT: Ande LICANT: Ande LICANT: Con- L | y Match<br>Local S<br>hes 41<br>3<br>3<br>450-763-<br>ence 257<br>RAL INFO<br>LICANT:<br>LE OF IN |
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LOCATION: (85)..(2142)
OTHER INFORMATION: 97% homologous to Homo sapiens putative p150, accession number OTHER INFORMATION: U93563, Smith-Waterman Score=3485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SIMILAR
LOCATION: (241)
OTHER INFORMATION: 100% homologous to Homo sapiens endoglycan, accession number
OTHER INFORMATION: AF219137, Smith-Waterman Score=1070.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACTITAAGCITATAGCGAIGACIGCCCGCITITCCAGICGGGAAACCIGICG
                                                  APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OP INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TILE REPERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR PLILING DATE: 2000-03-31
PRIOR PLILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NOS: 60736
LENGTH: 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450, 763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 13349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.2%; Score 35.6; DB 8; Best Local Similarity 82.0%; Pred. No. 3.3e-05; Matches 41; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.6; DB 8;
Pred. No. 3.4e-05;
     Sequence 13360, Application US/10450763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-450-763-13349/c; Sequence 13349, Application US/10450763; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
i_LOCATION: (1)...(1637)
CTHER INFORMATION: n = a,t,c or g
US-10-450-763-13360
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82.0%;
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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OTHER INFORMATION: 99% homologous to Cloning vector pBACe3.6

COTHER INFORMATION: levansucrase, accession number U80929, Smith-Waterman Score=1333.
US-10-450-763-25782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SIMILAR
LOCATION: (961)..(899)
OTHER INFORMATION: 100% homologous to Cloning vector pBACe3.6
OTHER INFORMATION: levansucrase,accession number U80929,Smith-Waterman Score=110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 8; Length 20795;
Pred. No. 3.7e-05;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURDAY HYSION AND AND AND POLYPEPTIDES TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 790C1P2/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PAPLICATION NUMBER: CT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 28400
LUMB TO SEQ ID NOS: 60736
SEQ ID NO 28400
LUMB TO SEQ ID NOS: 60736
SEQ ID NO 28400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8080 GTTTATTGCAATCATTGCCCGCTTTCCAGTCGGGAAACCTGTCG 8037
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CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: POT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CURECOM
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; Sequence 28400, Application US/10450763
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-28400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.6%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
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US-10-450-763-13360/c
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SIMILAR
                                                                                                                                                                                                                                                                                                            TYPE: DNA
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us-09-896-888a-10.rnpn

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Best Local Similarity 82.0
Matches 41; Conservative
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OTHER INFORMATION: 97% homologous to Homo sapiens putative p150, accession number OTHER INFORMATION: U93568, Smith-Waterman Score=3707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1514)..(1942)
OTHER INFORMATION: 100% homologous to Cloning vector pSacBII SacB, accession OTHER INFORMATION: number U09128, Smith-Waterman Score=768.
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  Gaps
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                                                                                           651 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.2%; Score 35.6; DB 8; Length 1942; 82.0%; Pred. No. 3.4e-05; tive 0; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                         APPLICANT: Hyseq, inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CT13/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 60736
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FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
9; Indels
0; Mismatches
                                             1 ACTIAAGCTIAIAGCGAIGACIGCCCGCI
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                                                                                                                                                                RESULT 6
US-10-450-763-4942/c
; Sequence 4942, Application US/10450763
; GENERAL INFORMATION:
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Best Local Similarity 82.0°
Matches 41, Conservative
41; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1514)...
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LENGTH: 2346
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LENGTH: 1942
Matches
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DB 8; Length 2346;

71.2%; Score 35.6;

Query Match

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LOCATION: (1)..(228) OTHER INFORMATION: 94% homologous to Homo sapiens Alzheimer's disease protein OTHER INFORMATION: 94% homologous to Homo sapiens Alzheimer's disease protein OTHER INFORMATION: encoded by DNA from plasmid pGCS22332, accession number W21578, Smith OTHER INFORMATION: Waterman Score=392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 100% homologous to Homo sapiens A human proliferation and OTHER INFORMATION: apoptosis related protein, accession number Y84901, Smith-Waterman JC-TRER INFORMATION: Score=838.
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                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 A PAPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/USO1/08631
PRIOR PLILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPREBUCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 13365
LENGTH: 2710
                                Indels
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82.0%; Pred. No. 3.6e-05;
tive 0; Mismatches 9;
                                                                                                                                                                                                                                                                 RESULT 8
US-10-450-763-23327/c
; Sequence 23327, Application US/10450763
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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NAME/KEY: SIMILAR
LOCATION: (1801).
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NAME/KEY: SIMILAR
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LOCATION: (1)..(840)
OTHER INFORMATION: 94% homologous to Cloning vector pZC320 SopA,accession number
OTHER INFORMATION: UZ6464, Smith-Waterman Score=1403.
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71.2%; Score 35.6; DB 8; Length 10771;
Best Local Similarity 82.0%; Pred. No. 4.8e-05;
Matches 41; Conservative 0; Mismatches 9; Indels 0;
                                                                                Length 5909;
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| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc
| TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
| FILE REPERENCE: 790CIP3/US
| CURRENT APPLICATION NUMBER: US/10/450,763
| CURRENT APPLICATION NUMBER: PCT/US01/08631
| PRIOR PILING DATE: 2001-03-30
| PRIOR APPLICATION NUMBER: 09/540,217
| PRIOR PILING DATE: 2000-03-31
| PRIOR PILING DATE: 2000-03-31
| PRIOR PILING DATE: 2000-03-31
| PRIOR PILING DATE: 2000-08-23
| NUMBER OF SECTION NUMBER: 09/649,167
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILLE REFERENCE: 790CT183/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTON
SQFTWARE: CUSTON
SQFTWARE: CUSTON
; OTHER INFORMATION: number U26464, Smith-Waterman Score=1509.
US-10-450-763-5236
                                                                                                                                Indels
                                                                           Score 35.6; DB 8;
Pred. No. 4.3e-05;
0; Mismatches 9;
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; Sequence 21710, Application US/10450763
; GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (1)...(10771)

OTHER INFORMATION: n = a,t,c or g
US-10-450-763-21710
                                                                           Query Match 71.2%;
Best Local Similarity 82.0%;
Matches 41; Conservative
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SEQ ID NO 28399
LENGTH: 20974
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CHER INFORMATION: 50% homologous to Cloning vector pZC320 SopA, accession number:
CHER INFORMATION: U26464, Smith-Waterman Score=40.
US-10-450-763-5677
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LOCATION: (5001)..(5864)
OTHER INFORMATION: 100% homologous to Cloning vector pZC320 SopA,accession
                                                                                                             Gaps
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                                                                                                                                                                                           1080 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1031
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                                                  71.2%; Score 35.6; DB 8; Length 2710; 82.0%; Pred. No. 3.7e-05; ive 0; Mismatches 9; Indels 0;
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                                                                                                                                                                                                                                                                                                                         Sequence 5-77, Application US/10450763
; GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TILLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT PEPLICATION NUMBER: US/10/450,763
CURRENT PILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTURE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SQOTWARE: CUSTOM
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Pred. No. 3.7e-05;
0; Mismatches 9;
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; Sequence 5236, Application US/10450763
; GENERAL INFORMATION:
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Best Local Similarity 82.0%;
Matches 41; Conservative (
                                                                                                           41; Conservative
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ORGANISM: Homo sapiens
                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                         RESULT 10
US-10-450-763-5677/c
     US-10-450-763-13365
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                                                          Query Match
                                                                                                           Matches
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APPLICANT: Wilson, W. David
APPLICANT: Wilson, W. David
APPLICANT: Boykin, David W
APPLICANT: Tidwell, Richard R
APPLICANTION: NOVEL COMPOUNDS THAT EXHIBIT SPECIFIC MOLECULAR RECOGNITION OF
TITLE OF INVENTION: A DIMER
TITLE OF INVENTION: A DIMER
TITLE OF INVENTION: A DIMER
CURRENT APPLICATION NUMBER: US/11/035,627
CURRENT FILING DATE: 2005-01-15
                                               NAME/KEY: SIMILAR
LOCATION: (7)..(387)
OTHER INFORMATION: 100% homologous to Bacillus amyloliquefaciens precursor (AA -
OTHER INFORMATION: 29 to 443), accession number X52988, Smith-Waterman Score=664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: EcrRi-PvuII fragment from plasmid pBS+, antisense strand
US-11-035-627-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3214 AATTAATTGCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 3165
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                                                                                                                                                                                                                                                                                                                                     Query Match 71.2%; Score 35.6; DB 8; Length 20974; Best Local Similarity 82.0%; Pred. No. 5.5e-05; Matches 41; Conservative 0; Mismatches 9; Indels 0;
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US-10-450-763-21773/C

Sequence 21773, Application US/10450763

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
PILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT PILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30

PRIOR PLING DATE: 2001-03-30

PRIOR PLING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 10/653,677
PRIOR FILING DATE: 2003-09-02
PRIOR PELICATION NUMBER: US 09/745,004
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: US 60/172,863
PRIOR PILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.2
                                                                                                                                                               FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(20974)

OTHER INFORMATION: n = a,t,c or g
US-10-450-763-28399
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GENERAL INFORMATION:
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70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative (
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ORGANISM: Homo sapiens
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LENGTH: 271
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PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PLING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 21773

LENGTH: 282

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

LOCATION: (124)

COTHER INFORMATION: 1004 homologous to Homo sapiens Amino acid sequence of a COTHER INFORMATION: 1004 homologous to Homo sapiens Amino acid sequence of a COTHER INFORMATION: 1004 homologous to Homo sapiens Amino acid sequence of a COTHER INFORMATION: 1004 homologous to Homo sapiens Amino acid sequence of a COTHER INFORMATION: =66.

SOTHER INFORMATION: =66.

US-10-450-763-21773

Query Match

Best Local Similarity 83.3%; Pred. No. 3.5e-05; BB 8; Length 282; Best Local Similarity 83.3%; Pred. No. 3.5e-05; Matches 40; Conservative 0; Mismatches 8, Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 8, Indels 0; Gaps 0; Matches 40; Conservative 0; Mismatches 67

Search completed: May 10, 2005, 09:51:26

Search completed: May 10, 2005, 09:51:26
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152 TIAATITITITIGGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 199
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Direct Submission
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Best Local Similarity
Matches 42; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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GSS 02-OCT-2001
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2 (bases 1 to 412)
2 (bases 1 to 412)
5 (bases 1 to 412)
Direct Submission
Submitted (01-0CT-2001) BBMI, Institut Pasteur, 25, rue du Dr.
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       BJ668962 BJ668962
AU069599 AU069599
BPB74955 BPB74955
BJ671717 BJ6771717
BJ6907999 GU002D02 O
BM419997 ROZOCI2 O
CB865576 HD10A15w
AG060720 Pan trog1
AG14861 Pan trog1
AG14861 Pan trog1
AJ57743 Arabidops
CF580104 P3225 S'U
B1977595 AG344b01.Y
B1977955 AG344b01.Y
B1977959 BPN trog1
AG109195 Pan trog1
AG045821 Pan trog1
AG045821 Pan trog1
CL096240 ISBN-2713
AG041822 CIT-HSP-2
CC961712 BOIDV76TF
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Anopheles gambiae GSS T7 end of clone 23P13 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito),
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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Anopheles gambiae
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Pred. No. 0.00023;
0; Mismatches 6

    .412
    /organism="Anopheles gambiae"

                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="PEST"
/db.xref="texton:7165"
/clone="23P13"
/clone lib="NotreDame1"
/note="end : T7"
                                                                                                                    AG134861
ATH517143
CF569104
                                                                                  CB865576
AG060720
AG043113
                                                                                                                                                                                BF703023
AG109195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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AL610451
AL610451.1 GI:15916636
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llarity 87.5%;
Conservative
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                                                                                           AQ080570 125 bp DNA linear GSS 20-AUG-1998 CIT-HSP-2358M2.TF CIT-HSP Homo sapiens genomic clone 2358M2,
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Venter, V.C.
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Wes of a random human BAC End Sequence Database for Sequence-Ready
Map Bullding
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1 (bases 1 to 174)
Adama; M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Venter, J.C., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. (bases 1 to 125)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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/clone="2358M2"
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TITLE

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Homo sapiens (Inducata) Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 177)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready Map Building

Unpublished (1998)

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Email: mdadams@208

Email: mdadams@208
Map Building
Unpublished (1998)
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Tel: 301 838 0200
Fax: 301 838 0208
Email: madadms@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
thtp://www.iigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Seg primer: M3-21
Class: BAC ends..
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'organia"Homo sapiens"

/mol_type="genomic DNA"

/db xref="taxon:9606"

/clone="2364M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Unpublished (1998)
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Exar: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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Adama, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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Seg primer: M13-21
Class: BAC ends.
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/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/clone_lib="CIT-HSP"
//note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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CIT-HSP-2368K7.TF CIT-HSP Homo sapiens genomic clone 2368K7,
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                                                                                                                                 Score 36.8; DB 8; Length 177; Pred. No. 0.00086; 0; Mismatches 7; Indels C
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85.4%; Pred. No. 0.00095;
tive 0; Mismatches 7; Indels
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Venter, J.C.
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RESULT 6 CO990192 LOCUS CO990192 372 bp mRNA linear BST 09-SEP-2004. DEFINITION UMC-pd3ov2-002-g02 Oviduct gilt D3 of estrous cycle pd3ov Sus

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escreta cDNA 3', mRNA sequence.

C0090122.1 Gr:13149466

EST.

C0090122.1 Gr:13149466

EST.

Sus scrote (pig)

Sus scrot
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source

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will be electroporated into DH10B bacteria. The day 12-14 endometrium library was synthesized by Dr. Bento Soares' laboratory (University of Iowa) and was cloned into the T3Typac vector as described elsewhere (Bonaldo et al., 1996). Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality (e.g. the presence of short poly4+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), ribosomal RNA clones (must be <1%), ribosomal RNA clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bloinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri-Columbia. Clone Requests to Clones should be made to the Director of the University of Missouri-Columbia. Bonaldo MF, Lennon G, Soares MB.

Normalization and Subtraction: Two approaches to facilite gene discovery. Genome Res, 1996; 6:791-806. 2. Jang H, Bivens NJ, Ries JE, Whitworth KN, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Frather: RS, Lucy MC (2001) Constructing construction and characterization of a normalized CDNA ribrary. Proc Nael Acad Sci, 91:9228-9232.

TAG_TISSUE=Oviduct gilt D3 of estrous cycle
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ORIGIN

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RESULT 7
CO947892
LOCUS
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REFERENCE 1 (bases 1 to 373)
AUTHORS Jang, H., Whitworth, K.M., Bivens, N.J., Ries, J.E., Woods, R.J.,
Forrester, L.J., Springer.G.K., Mathialagan, N., Agca, C.,
Fortester, L.J., Springer.G.K., Mathialagan, N., Agca, C.,
FORTHER TARGEST Generation and Analysis of Expressed Sequence Tags from JOURNAL Contact: DNA Core Facility (Swine Project)
COMMENT Animal Science - RS Prather
University of Missouri-Columbia
MG16 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573) 884-552
Email: porcine@rnet.missouri.edu
POLYA-NO.
Location/Qualifiers

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// Accession wis State Serrofa"

// Add Extefa tazon; 922"

// Add Exteraction the University of Missouris Genetic Source:

// Overlan tissue (whole ovary, dissected follicles, or

corpora lutes) was collected from crossberd piggs (Sus

scrofs demestica), frozen in liquid nitrogen shortly after

collection, and stored at 90 degrees Celsisus until RNA

extraction. The tissue from several individual pigs was

pooled for the purpose of RNA extraction. The specific

tissues collected wore fetal whole ovary; neonatal whole

ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing

follicles; Day 0 follicles; Day 5 small antral follicles

and corpora lutes aby 12 corpora littes and Day 12

follicles. More information regarding the methods can be

found at:

introper ordercution (Standard Protocol); All procedures

discussed in this section have been described in detail

introper ordercution (Standard Protocol); All procedures

discussed in this section have been described in detail

introper ordercution (Standard Protocol); All procedures

discussed in this section have been described in detail

introper ordercution (Standard Protocol); All procedures

discussed in this section have been described in detail

introper ordercution (Standard Protocol); All procedures

discussed in this section have been described in detail

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The librarie were constructed essentially as described by

suppressed of 21 landar by the procedure of a secretic tronic of the introper of section of the internal of section of section of section of section of short of the inter
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/dev_grage="Perinatal ovary"
/clone lib="pnatal"
/clone lib="pnatal"
/note="Vector: psporti; Funding: A grant from the Monsanto
Company to the University of Missouri. Genetic Source:
Ovarian tissue (whole ovary, dissected follicles, or
corpora lutea) was collected from crossbred pigs (Sus
scrofa domestica), frozen in liquid nitrogen shortly after
collection, and stored at -80 degrees Celsius until RNA
extraction. The tissue from several individual pigs was
pooled for the purpose of RNA extraction. The specific
tissues collected were fetal whole ovary; neonatal whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang, H., Whitworth, K.M., Bivens, N.J., Ries, J.E., Woods, R.J., Forrester, L.J., Springer, G.K., Mathialagan, N., Agca, C., Prather, R.S. and Lucy, M.C.
Large-scale Generation and Analysis of Expressed Sequence Tags from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 09-SEP-2004
Ea CDNA 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures
discussed in this section have been described in detail
elsewhere (Soares et al., 1994; Bonaldo et al., 1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
2. Jiang H, Bivens NJ, Ries JB, Whitworth KM, Green JA, Portester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci., 91:9228-9232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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UMC-pnatal4-004-e04 Perinatal ovary pnatal Sus scrofa cDNA 3'
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                                                                                                                                                                                                                                                                                                                                                                                                  73.6%; Score 36.8; DB 7; Length 373; 85.4%; Pred. No. 0.00098; ive 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
Miscrsity of Missouri-Columbia
MG16 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573)882-0428
Fax: (573)884-5552
Email: porcine@rnet.missouri.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                             library. Proc Natl Acad Sci, 5
TAG TISSUE-8mm ovarian follicle
TAG_SEQ-Not found"
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

RESULT 8 CO954011

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REPERENCE AUTHORS JOURNAL

TITLE

FEATURES

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Sequence locationing and upobsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded CDNAs was ligated to Sall adapters (Invitrogen-life conditions) and digested with Not1. The CDNAs will be size selected by passage through CDNA size fractionation columns (Invitrogen-life technologies). The CDNAs will be size selected by passage through CDNA size fractionation columns (Invitrogen-Life technologies). The CDNAs well size of the pSPORTI vector. The Not1 and Sall sites of the pSPORTI vector. Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be alst plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be alst), ribosomal RNA clones (must be alst), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spoilen, JE Ries, A Guillen, AA Khambati, RV Patel, Columbia. Clone Requests Requests for clones should be made to the Director of the University of Missouri-Columbia. Clone Requests Requests for clones should be made to the Director of the University of Missouri DNA core facility at: porcine@ment made south. Langenth Clite Columbia. Clone Requests (Soares MB).

Veriations: 1. Bonaldo MF, Lennon G, Soares MB.

Normalization and Subtraction: Two approaches to decine the Director of the University Charles Each Lange (Soares MB). Prather RS, Lucy MC (2001) conserved the presence of the Director of t
Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Priendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18148-013). Briefly, img of poly(A)+ RNA will be annealed at 37 degrees Celsius with 10mg of NorI-tag-d718 oligonucleotide (GCTGCTGGGGCCC-tag-T18) and reverse
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Jelene, L Su, L Lawton, A Efstrantiadis. 1994.
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TAG_TISSUE=Perinatal ovary
TAG_SEQ=Not found"
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Best Local Similarity 85.41
Matches 41; Conservative
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EST 21-JUL-2000

linear

mRNA

451 bp

BE403103

RESULT 9 BE403103 LOCUS

266

3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50 219 Traatreceraececreacrececerriceaereeeaaaacereree

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                                                                                                  Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Pooideae; Triticeae; Triticum.

E 1 (bases 1 to 451)

S. Dubcovsky, J., Faullet, C., Gale, M., Graner, A.,

Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A.,

Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J.,

Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P.,

Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.

International Triticeae EST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae

L. Onpublished (2000)

Contact: Jacquemin JM

Centre de Recherches Agronomiques, Departement de Biotechnologie

234 chaussee de Charleroi, 5030 Gembloux BELGIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS07H85 455 bp DNA linear GSS 02-OCT-2001
Anopheles gambiae GSS T7 end of clone 25H23 of library NotreDamel
from strain PEST of Anopheles gambiae (African malaria mosquito),
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Direct Submission
Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
  GBX Wheat Root Library Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="GBX002.C11"
/tissue type="root"
/dev_gtage="seedling, unstressed"
/clone lib="ITEC GBX Wheat Root Library"
/note="Vector: pUC18; 0.3-2.0 Kbp average insert size."
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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International Triticeae EST Cooperative (ITEC)
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                    cDNA clone GBX002.C11, mRNA sequence
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Location/Qualifiers
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/cultivar="Odeon"
GBX002.C11F990602#08 ITEC
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Fax: 32 81 61 04 59
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/tissue_type="Whole Plant"
/clone_lib="Arabidopsis_RT-PCR Products (CSHL)"
/clone_lib="Arabidopsis_RT-PCR Products (CSHL)"
/clone_lib="Arabidopsis_RT-PCR Products (tabliana whole plant tissue, provided by members of Rob Martienssen's lab, using TRIZOL. Primers were designed in Hypothetical genes and un-annotated regions in Arabidopsis that are conserved in Brassica oleracea located in the short arm of chromosome 4. PCR products were either cloned into pCR chromosome 4. PCR products were either cloned into pCR TOPO 2.1 vector (Invitrogen) and then sequenced using -21 M13 forward and reverse universal primers or treated with Exonuclease 1 and Shrimp Alkaline phosphatase and sequenced using the specific primers."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 591)
Aratari, M.S., Balija,V. and McCombie,W.R.
Arabidopsis RT-PCR Products (CSHL)
Unpublished (2004)
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Blochem. and Biol. Molec. of Insects, Institut Pasteur.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 455;
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500 Sunnyside Blvd., Plainview, NY 11797, USA
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/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.8; DB 9
Pred. No. 0.001;
0; Mismatches
                                                                                                                                                                                                                                             gambiae"
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:7165"
/clone="25H23"
/clone_lib="NotreDame1"
/note="end : T7"
                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="PEST"
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High quality sequence stop: 591.
Location/Qualifiers

    .455
    /organism="Anopheles

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="tk66a07"
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Fax: 516 422 4109
Email: mccombie@cshl.org
matches At4g04920
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Similarity 85.4%;
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(bases 1 to 655)
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AUTHORS
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AG125607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, T=1:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                  AG068743 . 641 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-059B24.F, genomic survey sequence.
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Pan troglodytes DNA, clone: PTB-041G18.F, genomic survey sequence.
AGO55437
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                       Gaps
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Direct Submission
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end seguences of Library PTB
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73.6%; Score 36.8; DB 7; Length 591; 85.4%; Pred. No. 0.0011; ive 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
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Pred. No. 0.0011;
0; Mismatches 7; Indels (
                                                                       3 TIAAGCTIATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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Best Local Similarity 85.4%;
Matches 41; Conservative (
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                  Local Similarity 85.4 les 41; Conservative
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                                                                                                                                                                                                                                                                                                             Pan troglodytes
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R.Site 1
R.Site 2
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Query Match
Best Local S
Matches 41
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Submitted (02-A05-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-1: Chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of PRIMERS
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Pan troglodytes DNA, clone: PTB-135016.F, genomic survey sequence.
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammālia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                          Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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Direct Submission
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                           Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
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                                                           Fujiyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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R.Site 1 : SacI
R.Site 2 : SacI
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan (E-maul:chimpbes@gc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, T=1:81-45-503-9111, Fax:81-45-503-9170, Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toroki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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                                                                                                                                                                                                                                                                                                                                              73.6%; Score 36.8; DB 9; Length 681; ilarity 85.4%; Pred. No. 0.0011; Conservative 0; Mismatches 7; Indels
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/db_xref="taxon:9598"
/clone="PTB-135016.F"
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'db_xref="taxon:9598"
'clone="PTB-127D11,F"
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: SacI.
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R.Site 2 : SacI.
Sequencing: -21M13
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Search completed: May 10, 2005, 07:25:15 Job time : 353.316 secs

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Run on:

Sequence:

Searched:

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unclassified.

I (bases 1 to 564)

Is Grigllattir.R.A., Theilmann, D.A., Pfeifer, T.A. and Hegedus, D.D.
Insect expression vectors
Insect expression vectors

A patent: JP 2001516225-A 1 25-SEP-2001,
THE UNIVERSITY OF BRITISH COLUMBIA

ON Multicapsid mucleopolyhedrovirus
PN JP 2001516225-A/1
PP 25-SEP-2001
PF 27-MAR-1999 UP 1998541010
PR 27-MAR-1997 US 60/049946, 28-JAN-1998 CA 2221819 PI
THOMAS A GRIGLIATTI, DAVE A THEILMANN, THOMAS
A PFEITER, DWAYNE D
PI HEGEDUS
PC C12N15/85,C12N5/06,C12N15/69/C12N9/22
CC Insect expression vectors
PT source Location/Qualifiers
FT source Location/Qualifiers
FT Source Location/Qualifiers
FT - 1.564
FT - 1.564
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AC121979 Mus muscu
CR361569 Danio rer
AP003376 Oryza sat
AC134482 Rattus no
AC134555 Rattus no
AC135655 Rattus no
AP005031 Streptomy
BD221352 Human gen
AY327402 Choriston
Continuation (3 of
AL939130 Streptomy
CCS597684 Sequence
CC6597684 Sequence
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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/note="ClaI site"
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/db_xref="GI:404519"
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Location/Qualifiers
1. 1429
/organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism=
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1 (bases 1 to 1429)

Wu, X., Stewart, S. and Theilmann, D.A.

Faracterization of an early gene coding for a highly basic 8.9K protein from the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

1. Gen. Virol. 74 (Pt 8), 1591-1598 (1993)
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100.0%; Score 177; DB 14; Length 1429;
Best Local Similarity 100.0%; Pred. No. 6e-41;
Matches 177; Conservative 0; Mismatches 0; Indels 0;
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Sequence 60 from Patent WO03042244.
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NPHTTAA 1100 DNA linear VRL 02-AUG-1993 Orgyia pseudotsugata nuclear polyhedrosis virus transcriptional trans-activator (IE-2) gene, complete cds; ORF, complete cds.
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                                               Klysner,S., Nielsen,P.S., Bratt,T., Voldborg,B. and Mouritsen,S. Novel immunogenic mimetics of multimer proteins patent: WO 0304244-A 60 22-MAY-2003, Pharmexa A/S (DK); Klysner, Steen (DK); Nielsen, Finn Stausholm (DK); Bratt, Tomas (DK); Voldborg, Bjorn (DK); Mouritsen, Soren
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                                                                                                                                                                                                                                                                                                                                                                                     /note="p2ZOp2F expression vector for insect cells" 561. .566 /note="HindIII site"
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other sequences; artificial sequences.
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480 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 539
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NYNSNFVTSTECNHAVCFKCYVSIVLSRAREAPSKCSICNRTTISCRAYNRDGYVETTDI
NYNSNFVTSTECNHAVCFKCYVSIVLSRAREAPSKCSICNRTTISCRAYNRDGYVETSTDI
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LLRQQLDVKZARLAHESNARLKLQKQNBTLSANNLSLQHQLNTQVIESRVKMEQFKRQ
HDEFNEKFKLSLS:
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rqravnlheavnrherlrrelgermtrsptllnyspsysptsprsrspdlimpedlop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF; homologous to the ACMNPV PE-38 gene; putative"
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PNSVVSCKFI KKTGDRTPACLQPMLALKTI QDRYMATEEEBATEPSFVI KNLQAQLDA
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                                                                                                                 2 (bases 1 to 4170)
Theilmann, D. A. and Stewart, S.
Tandemly repeated sequence at the 3' end of the IB-2 gene of the baculovirus Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus is an enhancer element
Virology 187 (1), 97-106 (1992)
                                                                                                                                                                                                                                                                              Original source text: Orgyia pseudotsugata nuclear polyhedrosis virus DNA.
1 (bases 1 to 4170)
Theilmann, D.A. and Stewart, S.
Molecular analysis of the trans-activating IE-2 gene of Orgyia
pseudotsugata multicapsid nuclear polyhedrosis virus
Virology 187 (1), 84-96 (1992)
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1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACGGCAGCCGGACGCAACTCCT

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/kriamslation="MDAAGSLSREVADCASPFAMAIVMDYVPCPDLFBTLQTQ
GALDNALVVNIVRQLCDALNDLHNATGYIHNDVKLENVLYFGARDRYYLCDYGLCKRE
                                                                                                                                                                                                                                                                                                                                                                  OPU75930 131995 bp DNA circular VRL 25-MAR-2003 Orgyia pseudotsugata multicapsid nucleopolyhedrovirus, complete
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MRRRQQYNDPAALKNVRNLMARDFVFCLTRFNFECRSTDYKQIAKHSFLASRHDYI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome
Virology 229 (2), 381-399 (1997)
97271300
1 (bases 1 to 131995)
Ahrens,C.H., Russell,R.L., Funk,C.J., Evans,J.T., Harwood,S.H. and
Rohrmann,G.F.
                                                                                                                                                                   600 CGAGGCGCCCGTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 656
                                                                                                                                   121 CGAGGCGCCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-OCT-2000) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA Sequence update by submitter on Oct 26, 2000 this sequence version replaced gi:2934903.

Location/Qualifiers
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Direct Submission
Submitted (23-OCT-1996) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA
3 (bases 1 to 131995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orgyia pseudotaugata multicapsid nucleopolyhedrovirus
Orgyia pseudotaugata multicapsid nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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/note="ORF1; pk-1; similar to AcMNPV ORF10"
/codon_start=1
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/note="ORF2; similar to AcMNPV ORF9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="1629-capsid"
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complement (8180...9142)
/note="ORP12; similar to AcMNPV ORF13"
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COMPLEMENT (9094: 9225)
/note="ORF13; lef-1; similar to AcMNPV ORF14"
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AQCEAYLYNKSISDVHYWCATAFWLFB
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SFADCVRRAVHMYIGDAREDLVLRYWPDVDRDVFCNANKQJRAPFSYNYKGGDYSRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MVFLIIALTLLATGARAASILAVLPTPAYSHHVVYRAYVHALVK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCHNYTVIKPOLLDYAVODECGRVEQIDADMSAQOYKKLVASSGVFRKRGVVADETTV
TADNYMGLIEMFKDQFDNANVRRFLSTNRTFDAVVVEAFADYALVFGHLFRPAPVIQI
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                                                                                                                                                                                                                                                                                                                     FPDRWHEYTACGAVI EGTRLLCFKVPLNAELFEYVTSDEDRWTAASVLARHSALGAVI
DLINTARYYDGAQMYKMGLLYKKI RVPGRAVPDDDI VAEFI ETVDEFFRRCPTMLVAV
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PIRHALGLPVGDHIHVYCEAAPTCAALPNAMPALYDYMVRRIGEGKRVLVHCYAGASR
SAALAVYYLMRSRQMPYQDALNAVQSKRRVAINDHFVRFLATRCSYRFVNDELKFQIV
                                                                                                                                                                                                                                                                                       translation="MLTSRRWAVIYTRTSERNCGGAWCTNGVRRRQVHLPSVRARAM"
                                                                                                                                                                                                                                                                                                                                                                                HWTHGLNRSGYLVCRYMVERLGVSPTDAIARFETARGHKIERTNYLQDLLARKHVRGQ
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/product="ecdysteroid UDP-glucosyltransferase"
                                                                                                                                ORF1"
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                                                                                                                             note="ORF10; ptp-1; similar to AcMNPV ORF
/codon_start=1
/product="protein tyrosine phosphatase 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  6819. .7814
/note="ORF11; similar to AcMNPV ORF11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to AcMNPV ORF16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="late expression factor 1"
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100.0%; Pred. No. 5.2e-41;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rooloorikacsagclaggtpptsk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="unknown"
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/db_xref="G1:1911257"
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/protein_id="AAC59011.1"
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/db_xref="GI:1911260"
                                                                                                                                                                                                                            /protein_id="AAC59009.1"
/db_xref="G1:1911256"
                                                                                                  .6791)
                                                                                                      complement (6129.
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/note="ORF15; si
/codon_start=1
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Best Local Similarity 100.0
Matches 177; Conservative
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IARYLLAECGĀVLVIDHPLDVFGETEEGVNELLEVQRINAGGDL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MGASQNSEQKILKLFYRWSSQTGAALDDEKDLHCLYDLERFVGA
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AREKEIVDRIHRLQLKQDSLLKQDRLKKR"
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                                                                                                                                   RNLNSVLÄR I BALLRVDVVNDAEVNVLSGDFYEEYSKY I SYQOTFAQTPTASASQOTQ
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SDEFVYVPGKERAVPDTRFKPPVPPKPEHLKSRPSSVATNAAGATPVAPPPPPPSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MPDYSYRPTIGRTYVYDNKYYKNLGSVIKNAKRKKHLLEHEEDB
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INNILIDAMVAETNKWAGDNRSALLDQIKQGKTLKKTQPADGAPATDPRSTLLSEIRQ
                                                                                                                                                                                                                                                                                              GKTLKKLRKI EDQSSTQTLLKDVDTTDKTKTILKNFVTNIDRISKQEQEEKDRLDTIT
KRRPAVEHTDGNSTGNNSDDWRDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MRKNNGASQYPEHLTTVHKRHRLQLSCVWCDDQRSWDPHSAKGL
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/note="ORF6; lef-2; similar to AcMNPV ORF6"
/codon_start=1
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db_xref="GI:1911255"
                                                                                                                                                                                                                                                                                                                                                            complement(2533. .3270)
/note="ORF3; ph; similar to AcMNPV ORF8"
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/note="ORF8; similar to AcMNPV ORF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4742. .4975)
/note="ORF7; similar to AcMNPV ORF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNRFLEAGDRAPAVIVKAAANGGQHSSLICDKV
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db xref="GI:1911250"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC59004.1"
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/note="ORF9; ptp-2"
/codon_start=1
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                                              xref="GI:2934904"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFEHMFCCLRIYVQQKIKH"
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       fumiferana multicapsid nucleopolyhedrovirus genomic region encoding
the regulatory genes pkip, p47, lef-12, and gta
Virology 271 (1), 109-121 (2000)
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                                                                                                                       8 (bases 1 to 129609)
Caratens, B.B., Liu, J.J. and Dominy, C.
Caratens, B.B., Liu, J.J. and molecular characterization of the baculovirus CfMNPV early genes: 16-1, 16-2 and pe38
Virus Res. 83 (1-2), 13-30 (2002)
                                                                                                                                                                                                                                                                                        9 (bases 1 to 129609)
de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krall, P.J.
Complete Genome of Choristoneura fumiferana Multiple
Nucleopolyhedrovirus
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-2002) Department of Microbiology, University o Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 (bases 1 to 129609)
de Jongy,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B. and Krell,P.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-MAY-2004) Department of Microbiology, University o Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B. and Krell,P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence update by submitter
On May 13, 2004 this sequence version replaced gi:30269978.
Location/Qualifiers
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complement (1862. .2092)
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protein id="AAP29797.1"
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Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
viruses isolated from Choristoneura fumiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
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Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene
expression in insect cells
Virology 217 (2), 564-572 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xie,W.D., Arif,B., Dobos,P. and Krell,P.J.
Identification and analysis of a putative origin of DNA replication
in the Choristoneura fumiferana multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                          circular VRL 27-MAY-2004
                                                                                                                                                                                                                                                                                      129609 bp DNA circular VRL 27-MAY-200. Choristoneura fumiferana MNPV polyhedrin, complete genome. AF512031 AF177329 S78506 S81690 U10441 U18677 U26676 U26734 U53854 U57401 U59008 U70432 U72240 X65395 S46001
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                                                                                                                                                                                                    128642 CGAGGCCCCTCCCCCTTATCGCGCCTATAATAAAAACCGCAAAGGATCTGGTAAA 128698
                                                                       TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
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Identification and molecular characterization of the Choristoneura
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                                                                                                                                                                      CGAGGCGCCCCTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome of
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Nucleopolyhedrovirus.
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Lee,H.Y., Arif,B., Dobos,P. and Krell,P.
Identification of bent DNA and ARS fragments in the Choristoneura fumiferana muclear polyhedrosis virus Virus Res. 24 (3), 249-264 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyhedrosis virus genome
Virology 209 (2), 409-419 (1995)
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Virology 223 (2), 396-400 (1996)
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Liu, J.J. and Carstens, B.B.
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Pseudomonas putida KT2440

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Bacteria; proteobacteria; Gammaproteobacteria; Pseudomonadales;

Beaclan, M., Paellsen, I., Weinel, C., Dodson, R., Hilbert, H., Fouts, D.,

Gill, S., Pop, M., Martins Dos Santos, V., Holmes, M., Brinkac, L.,

Beanan, M., DeBoy, R., Daugherty, S., Kolonay, J., Madupu, R.,

Rizzo, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, J.,

Hoheisel, J., Straetz, M., Heim, S., Kiewitz, C., Eisen, J., Timmis, K.,

Bobesterhoft, A., Tummler, B. and Traser, C.

Complete genome sequence and comparative analysis of the

metabolically versatile Pseudomonas putida KT2440

AL Environ Microbiol. 4 (12), 799-808 (2002)

CC 2 (bases 1 to 300363)

CC 2 (bases 1 to 300363)

Nelson, M., Martins Dos Santos, V., Holmes, M., Brinkac, L.,

Beanan, M., DeBoy, R., Daugherty, S., Kolonay, J., Madupu, R.,

Holtzapple, E., K., Kosack, D., Moestl, D., Wedler, H., Lauber, T.,

Rizzo, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, T.,

Rizzo, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, T.,

Rizzo, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, T.,

Rizzo, M., Lee, K., Kosack, D., Moestl, C., Eisen, J., Timmis, K.,

Duesterhoft, A., Tummler, B. and Fraser, C.

Direct Submitted (05-NOV-2002) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

Location/Qualifiers
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GHGSTGAATVTRAPEPERTSEKERELK
GHGSTGAATVTRAPEGEDTRLEYVPRABMAANIGARLMYYYTVTRAGETRTSEKFELR
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GQDVTHILRPPTEATYDEYSOGVIKAYLPKQPLGNILDLGKDPRLTVSASFDDGETWR
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Pseudomonas putida KT2440 section 8 of 21 of the complete genome.
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2024. .4489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus tag="PP1883"
78. .1985
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/transl_table=:
                                                                                                                                                                                                                                                                                                                 AE016781.1 GI:26557025
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JOURNAL
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                               RESULT 7
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/note="more property | Act | Opto" |
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/protect="protein tyrosine phosphatase 1" |
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VDEFQDRCFTMLVGVHCTHGLNRSGYLVCRYMVDKLGVSPADAIIRFBEARGHKIERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="AAP29801.1"
db_xref="GI:30269985"
'translation="WAMLKTFLLICVSSAALSVKVTTINNVLYTVNDTQKTIAVKQVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="WYDANGIDKY!FVGGYYGDDKAMLQF!KKYDIASV!SL!NADVG
PIRQALGLPAGEHIHVYCEDAPTCVALPNAMPALYEYMTRR!GEGKRVL.HCYAGESR
SAALVVYYYMRSRQMSYEEALS!JVKNKRRVA!SNHFVRFLASKCSYKFVNNVLK!RVS
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LCANVQLALAEIDKYAPLEKRVSIGNNIFALDTIADIPSNALDDFQTIIYBGFKDFVD
MNNLAHVADVFDPDPKIKAEGWWYYKFCVLTYMHRLTVNAVPTELWTRLQDAVIKFVQ
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VDRYTVIPHBHKNRMYYGQLYSFALLANDSLALDY YIGAPIFEKERMYSVITARHEDYK
NKLVIYPPUTGISAGLUSGGINFDLQILTQKKLLEGSSVYGKNQLPYKALKDYAISTNR
NKNLFKGLPRNVAVFYNERDITIALVEGFFEIDRIRLSGPLILRNIKQQ"
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KDFGRLCKETYTDLRAEADLLYINATTDEKKNALFDLLCCVNAADLDVDCYDYIVDNF
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CNRFLDGVDKAPAVIIKPAAAGQHSSLICDKV"
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FrpddrdallaacmvnvQaygadGtirlQptliyyrvCrnfravadvpapddhfiar
YlmpecGtplvidhplhvFgdteegvnellevQrinaggdl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MDRNIKKNAVTDTWIFKMCIHYTRTGIHHPCLSNSFVKRPVYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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19.9%; Score 35.2; DB 14; Length 129609;
Best Local Similarity 92.5%; Pred. No. 11;
Matches 37; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="protein tyrosine phosphatase 2"
protein id="AAP29802.1"

db_xref="GI:30269986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codom_start=1
product=-baculovirus repeated ORF"
protein_id="AAR29800.1"
db_xrefi="GI:3026988"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (2896. 3699)
/note="ORF7; Ac136/Op132"
/codon_start=1
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/note="ORF10; Ac11/Op11"
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'db_xref="GI:30269988"
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/db_xref="G1:30269983"
                                                                 protein_id="AAP29798.1"
db_xref="GI:30269982"
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/note="ORF8; ptp2; Op9"
/codon_start=1
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                                                                                                                                                                                            2137. .2568
/note="ORF5; Ac4/Op8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHTVLINNNYAQDAPQFAI"
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'product="unknown"
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product="unknown"
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/note="ORF6;Ac2"
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161056 GGCGTACCGGGCGAGCACGGCAACCTGCTCGGTGTCGAACCACTGCTGTACCCCCGGCGAAC 160997
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SAARDRONLERYTRHEIDPREGQAAKVYREYEPGRESSEISWBOGLDULYKVP
EDYTYKSIQTQEVRRGOSVRTITRTERREHLLTEQATAGCDKLLQAFTRYADNGANFES
QEPYTYKSIQTQEVRRGOSVRTITRTERREHLLTEQATAGCDKLLQAFTRYADNGANFES
QEPYFQLPHDETQRWSLISNPSRQREEKRYTRYDSHGNVLTRLLPNOVLETNVWYSAE
ERDBEHGFYRNLKTRYVQFAATGHGAAATLTQOPROPRALLESETL
SESGSAPGTFLEKISTYQESSAERFSYGYGYVSYFGVDGGSPFDTLTHYGYSLL
DDERALQTVEKLVGVDGESKTITLRHALDTGEPLLNLDDDGVEIRYYDALRRVYTREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAPGKPFEAERNYKYFLCAYDNEQAQOMAYDVKQVETHTLLDGLSRPPFEERADDKDSA
TYGALLRP IT RARKYDELDQU'USETE IDMLGBOLLELTSHI SYDDWGGRYA'LLNPDGTT
QVEET DQVAAFTDGPWHRAWREVVERBVGGT ITETWYNLPEKPVR I ERPALDGSTS I SLJ
NNDYDGLGRLSREAQGSGAGQR'VVEYRYDAFDR VREBRLADR'NYTYRTAGHSRNDL
VAS IKKGWITESAAVLLGSQVFDGLERRTVATTGGREQTFEYDPGERQPHWYKAPDGTR
I EYQYRPALGEEPVLAULSGREAKKEYDLKNARLTHCEEPGDDENGSCYLLDRSHFLSN
GEVKRESRTVDGEAFSMYYDYSFRSRLAAYDVJGQTQLYDFDDVGRLEKTTLLARPEP
                                                                                                                                                                                                                                                                                                                                                              /translation="MMSTSTSVHSNAFNFSSYIESGVDPRTGQYTVSIRLPELQGNDL
QGPGFBLALPYSPLNGEDSGFGKGMNLQLTQVRKHIVTLSSGETYKITGKSSVTGRLE
MKEQKLRQFDLYEDPPGPGGAARPRVEHRSGLVEVLEVMGSGEGEVALPVELHSPLGH
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FYPEDGUYQYTAQDYDEFDCLKSRILKGRPKGSDESQATLAHETYVDYDRRGRLQIY
TCDGPRAPVDPSGGTIARQIFGFDGLDNILSVITYRPDGSWQRTLYEFRUSDPAQMSR
IIPPDALLETYDVDHDLEBELFKIVKYDPQLAIDLHYDGNGNLISDEQGRVLTYDGLNR
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VHVRDLWTLYVPRDARIGTTIGTPELFBATLDQNNLALLCRTYGBRINFNFQAARGVH
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LLGPATLATFRHRITLVKTGDLPPGEHQLDGVLVTGHLDWGGFGKVLEYTLRAMVIQT
QCDASADVSANPVDLGEWSVNDFTGPGFTTPPAAFQVRLSNCQVDPDPGNETLATIEL
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FOARFROTEPNSSLRTGLAKGALNFTIRYR"
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                              10329. ..14201
/locus tag="PP1887"
/note="identified by match to TIGR protein family HMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="PP1889"
/note="identified by match to PFAM protein family HMM
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/locus tag="PP1888"
complement(14251. .15345)
/locus tag="PP1888"
/noces-similar to SP:P42185; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.8; DB 1; Length 300363;
Pred. No. 14;
0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                   /producT="hypothetical protein"
/protein_id="AAN67506.1"
/db_xref="GI:24983396"
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/product="fimbrial protein"
/protein_id="AAN67507.1"
/db_xref="G1:24983397"
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locus_tag="PP1887"
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/transl_table=11
                                                                                                                                                                                   start=1
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                                                                                                                                                    TIGR01643"
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                    APMESDDAADVDGALVGLVAMGPSNGPONMPGPEYRYLIPDDNGDYSATVLLDKAWVA
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LSEFFHVLWGYAAPWYSPSSBRGAPAARALAKDLELDYMBELIDKTIKLNFGG
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VEGSSDDPGHPDQHTHGLYLAPGATGIEGEFTKVRVTATVPGGGFASSALLTVVKNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVSPLLSVCQVGDEGVSLKADSVAEGPLQWR I LGASPHGRLAQESGTANRY I PGENLP
DKSP I VEEVEVRNSLTNEHRTLCI VTQMTLKRPSDVVVDKRDEQHARVWLSI HFSEAS
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QPLLSVTFEHDEVRQHWKSHCTLTFTYKPKPTGPLYSRTATFQFDLQTVFTLNAPASP
EESAGCMLLGQVLWPWQAAEVTEVSGLPSDTPSDLREEIYAFVAFLVKQAVLEGLARE
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LEVTVETMQADGQDYKLCLDEIASIALFDRSGMKIPPLCGDGIDSGSGNVWRTNLKPN
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EPLPKFVSFDPDSKPLIDGVEREVSSVYQPGLLAIVNYRRRDLPFNRTSDHRALFEKL
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GRFFKEVLSGLGSRAGVYPLADFKALSGNPYLAVRHSSKADGKSALVIPAGI
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HTFSVEPPREGLTWSLEALPGTVGDLGR I DPASGEYRAPPAHAMAGKFVRVR I I ATDP
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VAEGDGRRCTYTAGSKVDANVAYVLDQVRVQNRETSESRSIYVLVRQRRPELVIDVKQ
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IPGSVFILEGHLILPLPLSLHFDAARRAASPTGLRVATSPSIGG"
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VERSION KEYWORDS SOURCE ORGANISM

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COMMENT

RFERENCE

DEFINITION

RESULT 8 AC121979 ACCESSION

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The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/67 mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="tRNA-Cys"
note="Likely pseudogene (HMM Sc=39.91 / Sec struct
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Location/Qualifiers
1. 155274
                                                                                                                                                                                                                                                                          l. .1552/4
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4855_ .4982
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788. 936
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5316 . 5565
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http://genome.wustl.edu
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                                               SOURCE INFORMATION
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                                                                                                                                                                                                                                          FEATURES
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                                                                                                                                                                                          AC121979 155274 bp DNA linear ROD 13-NOV-2003
Mus musculus BAC clone RP24-289L14 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
3 (bases 1 to 155214)
4 (bases 1 to 155214)
5 (bases 1 to 155214)
6 (bases 1 to 155214)
7 (bases 1 to 155214)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 155274) McPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-NOV-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 155274)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WIGSC Web site: http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 155274)
McLellan,M., Cotton,M., Doebber,A. and Schatzkamer,K.
The sequence of Mus musculus BAC clone RP24-289114
Unpublished (2001)
2 (bases 1 to 155274)
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Contact: submissions@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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AC121979.3 GI:24476151
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                        CGAGGC 126
                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R
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note="Likely pseudogene (HMM Sc=33.79 / Sec struct

/rpt\_family="MaLR'

9947. .10098 /rpt\_family="B4" 10110. .10490

Sc=-6.89)

repeat\_region repeat\_region

MAPPING INFORMATION:

Appping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see

restriction digest

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45478 CCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTCGCCGTGCCCCTGCCCACCACGG 45537
                                                                                                                                               CR361569 17-OCT-2004 Danio rerio clone CH211-99120, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-0CT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 11, 2004 this sequence version replaced gi:51592229.
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 179571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 175712 bases at least Q40
Consensus quality: 175324 bases at least Q30
Consensus quality: 176324 bases at least Q30
Insert size: 178471; unw-of-contigs
Insert size: 179905; 5.5% error; agarose-fp
Quality coverage: 7.91x in Q20 bases; sum-of-contigs Quality
coverage: 8.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently tonsists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
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18311: gap of 100 bp
33141: contig of 14830 bp in length
33241: gap of 100 bp
37691: contig of 4450 bp in length
37791: gap of 100 bp
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of 20408 bp in length
100 bp
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of 45661 bp in length
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contig of 6832 bp in length
gap of 100 bp
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of 7847 bp in length
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of 9526 bp in length
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of 3824 bp in length
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of 2169 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
                                                   45538 GACAGAGCGTCCCCTCTCC 45562
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                                123 AGGCGCCCGTCCCGCTTATCGCGCC 147
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CR361569.5 GI:54035037
HTG; HTGS PHASE1; HTGS DR
Danio rerio (zebrafish)
Danio rerio
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                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
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JOURNAL
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/note="Likely pseudogene (HMM Sc=20.93 / Sec struct
Sc=-0.89)"
                                                                 note="Likely pseudogene (HMM Sc=33.19 / Sec struct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.6%; Score 33; DB 10; Length 155274; 51.7%; Pred. No. 48; ive 0; Mismatches 70; Indels 0;
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3. .12290
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_family="RMER6B"
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5. .17489
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rpt_family="RMER6B"
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6353. .16501
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/rpt_family="ERVL"
17672. .17818
/rpt_family="Alu"
                                                product="tRNA-Ser"
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family="ERVK"
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rpt_family="MaLR"
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19415. .19480
/rpt_family="B2"
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18962, .19079
/rpt_family="B4"
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6183. .16352
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17406. .17489
/rpt_family="L2"
17585. .17934
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/rpt_family="B2"
11349. .11370
                                                                                                                                                                                                                                                                                  family="Alu"
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rpt_family="L2"
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rpt_family="B2"
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1043. .11114
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family="B2"
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Augmented (07-wak-2001) Taxujl Sasaxi, Natlonal Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affire.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Jul 17, 2002 this sequence version replaced gi:20975425.
Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, as well as SplicePredictor (October 1998 version). The genomic sequence was searched against (October 1998 version). The genomic sequence was searched against (October 1998 version). The genomic sequence was searched against (KfP://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at KGP. Protein homologies of the coding regions were searched against the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein.' A gene without of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.
The orientation of the sequence is from Milzev to -21Mil of the BAC clone. This sequence of OsymBa0014K08 clone has an overlap with P0439E07 clone (DDBJ: AP003768) at the position 1 to 45,852 of 5' end and no verlap with P04491E1 clone (DDBJ: aP003768) at the position of this entry is available at http://rgp.cha.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                   Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,
Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Masukawa, M., Azikawa, K.,
Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M.,
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Azita, K.,
Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,
Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Ito, S., Ito, T., Ito, Y.,
Ito, Y., Iwabhuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,
Kikuta, A., Kobayashi, T., Mukai, Y., Nachita, K., Machara, T.,
Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,
Nakama, Y., Nakamichi, Y., Nakamura, M., Namiki, N., Nagishi, M.,
Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T.,
Shomura, A., Song, U., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K.,
Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K.,
Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,
Yano, M., Jiang, J. and Gojobori, T.
The genome sequence and structure of rice chromosome 1
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3405. .3547,5098. .5199,6055. .6167,6605. .6690,7352. .7491))
/gene="OSJNBa0014K08.1"
                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
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/cultivar="Nipponbare"
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   clone:OSJNBa0014K08
                                                             AP003376.3 GI:21902027
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                                                                                                                        SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTAT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 AGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 179571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
154564: contig of 19806 bp in length
154664: gap of 100 bp
179571: contig of 24907 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174954 CCCCCCAAAATCTACAGCATGGAGATTCAGGTTAAA 174919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.5%; Score 32.8; DB 2; Ilarity 50.6%; Pred. No. 54; Conservative 0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 CGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly fragment:00502
fragment chain:1"
3242." 37691
/note="assembly fragment:00073
fragment chain:1"
37792. 44623
/note="assembly fragment:00179
fragment chain:1"
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00485. 98331
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90485. 102055
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fragment chain:1"
102356. 111881
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111982. 114150
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114251. 134568
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fragment chain:1"
114251. 134568
/note="assembly fragment:00751
fragment chain:1"
134759. 134564
/note="assembly fragment:01385
/note="assembly fragment:01385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment:01746
:ragment_chain:1
                                                                                                                                                                                                                                                                /clone_lib="CHORI-211"
1. 1821
1. 0. 1821
Fragment chain:1
clone_end:SP6
                                                                                                                                                    /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                              clone="CH211-99I20"
                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector_side:right"
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18312. .33141
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Best Local Similarity
Matches 79; Conserval
   134759
154565
154665
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APD03376
LOCUS
DEFINITION
                                                                                                                                 source
                                                                                               FEATURES
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148476 AAGGCCTCGCGCTCTTGTCCGGATTCCGCTGTCACGTTGCGCCCAGCCGCTGAGGCCCCC 148535
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/db.zef=[01:12190203]

/db.zef=[01:1219020]

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/d
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEALRSAAVAFGCFQVVGHGVDRSLVSAALRHVAAATARAATPEPEEVEVNGDDENGE
EMWWSPGDGGGEMAGNWALQSGASHFRNTADALFIQLEQTATKIMDVLQRGGAVATQS
IAGADTNGSLLCIRKHRRQDDRSGGASGPIRHDDILRMLVRSSRCSRALALHLCPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35132. 35437)
/gene="CSJNBaO014KO8 6"
complement(join(31081. 31242,31391. 31579,31787. 31815,
31903. 31993,32132. 32306,32410. 32549,32638. 32770,
3508. 33574,34086. 34243,34332. 34405,34496. 34609,
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AVGPSLDAKSCTFKHICRDYSGERTLCVSVIENRRFAPVSLDVQNKREMVNVLQCLDI
SIFFPC"
                                                                                                                                                                                                                                                                                                                                                                /translation="MATASVYTYLQRPRELPVPEFRAPPPSPVTGVLTSSSSGSLAYG
ECPDSNEDDEIGRFLRRSARVPVLRLPERAVPRKKKAAWAPPVIDVRLLALPEAGGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAFHIFSRRGWSRFRPMDGAVVVTVGDQLQACNGGLYKSVAGKPAYSNDDLRGNGGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVASAELFYCFPSAGTAAGKASEVLSADAGKIIPLNLQFMVAACLVLGYHFLLSSLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join(31081. .31242,31391. .31579,31787. .31815,31903. .31993,32132. .32306,32410. .32549,32638. .32770.33508. .33574,34086. .34243,34332. .34405,34496. .34609,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 GTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148416 GTGACAGCGGACGTACGTAATGTGGTTGGAATCTCGCCCGGTCGAAATTCCTTGGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="contains ESTs C72949(E2532),C72949(E2532)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVSAQSAAAYVMLASSECDLAYPDYRAVVKIFNGYRS"
join(39834. .39907,40580. .40722,41299. .41408)
/gene="OSJNBa0014K08.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(39834. .39907,40580. .40722,41299. .41408)

/gene="OSJNBa0014K08.7"

/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32.4; DB 8; Length 177263; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                 .29650)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
             .28537,28795. .29152,29378.
                                                                                                 .29152,29378.
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                                         /gene="OSJNBa0014K08.5"
join(27978. 28537,28795. 29
/gene="OSJNBa0014K08.5"
/note="hypothetical protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                            /proteIn id="BAC05581.1"
/db xref="GI:21902032"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="OSJNBa0014K08.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon start=1
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Similarity 53.1%;
69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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AC134482/c
             gene
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                                                                                            CDS
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    .6167,6605. .6690,7352. .7491))
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAIAHLKRCGFYLEKLAKKGRGNSPQRRGGAPRRLRVPTGNEEDDPPPLAPFALPLGR
QWCCCFGPAPPAGAREVRPPRLTWPPRRHPGCPATTPSRHRGLDDPPRHGLAPGGQAE
RRPPPPRFGRPRRAAAIRRLRPPLTNRLYAEPQLSAASAPVPGRPSRSRPPPRRLATG
                                                                                                                                                                                                                                                                   /translation="MARPDWILERERRQVEQILELDMEELQVEEVDDAGSSSSSEVDT
FLRNTHGDGGSRTSEALAFNTSVVSLPTCDGGVVLFPEAILPIRVVQPRSLTAVDKAV
NHVDAPCMIGVIHHIKQLDDGSSNVVTRGQNRFRLRRRWIDADDVALISRRSDGPVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKGILADDRLAKKPSRQYSMEKGSATNRAIPDFRSAAAMSDANRRARRRSPCHARNTR
NGTRRAGARPDPEPSRQPIRVLGGRSLSVDETWVTSPAAAVFLRHGETRAPAFALGTA
GRRRGEDDMSVIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLDGFNVCI FAYGQTGSGKTYTMSĞPGTSREDMGVNYRALNDLFDI SLSRKNÄFSYES
NRAVGSTALMERSSREHSILTYHVRGLDVKNGSTSRGCI-HI. IDIAGSSREVERSBATGD
RLAGQQHINKSLSALGDVI FSLAQKNAHVPYRNSKLTQVLQSSLGGQAKTLMFVQINP
DLESYSETI GTLKFRENVSGYLFSLAQKNARNEKDI KELLEQVASLGTDT LAKDMETBG
LQLLKSKSPNSMTDRNGSNLLAQSTSSTGLSSL-PVASQQNQQLSVYTLFPLADTGLAG
SVEARABDNASDDGCSVGETEYSPAGASETSAERAYVLILFSFISCAKPSCACDTSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="MRSMFLPVLPLRACGTGTTAPVPPPTASLRRELALSPNLPARGG
VAGQPNAATREAPAAAVSSARRVVVVSPSLARRRRTRPPPPPPPPLLFSPRVFSASPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGLI PRMRSLRLRSGRRRGESGGDQAGALI LSWVDANYRGYLDEQFCQVEDLQDEASP
NFVEEVVTLFFKDSGRLMSNI EQALCMRSFQKVKREHAVLRQKLESYFQLCSCTWAEB
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YLINGEALCYVADKLMPGVLEGTWGGYASDQRSNVKKFLSVVAEMGLPGFGVKDLEEG
SMSSIVECLLALKDNVATQLGGHISNSTAKTPIRRKLELRETDGPVLSVATPGKRYPK
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BSIERKRGBIPHRVNHLLRNYIQEIEHRIGIQADHIRNQNSIIKTREDKYRSKIKTALE
TLVMCTTHERNEMAINRLENDEKTKLDEKRKLGEQDMIRLIRBKENDANIIASLHQE
MQVMNRWHEQPRHDLKGLVDDAARNYHKVLABROQKLFNEVQELKGNIRVYCRVRFPLGE
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GLLREMAGLSSR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHHDRMPSRHIRPSRAAAGGIQAREGRIRPWGLRIRRLLPTLPP"
join(8072. 8086,9178. 9387,9474. 9671,12990. 13120,
14072. .14144,14960. .15376)
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join(8072. 8086,9178. 9387,9474. 9671,12990. 13120,
14072. .14144,14960. .15376)
/gene="GSJMB40014K08.2"
/gene="GSJMB4014K08.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="putative kinesin-like protein"
/protein id="BAC05580.1"
/db_xref="G1:21902031"
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join(16191. .16218,17138. .17280)
/gene="OSJNBa0014K08.3"
3405. .3547,5098. .5199,6055.
/gene="OSJNBa0014K08.1"
                                                                                            'note="hypothetical protein"
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                                                                                                                                                                                /protein_id="BAC05577.1"
/db_xref="GI:21902028"
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/db_xref="GI:21902029"
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/db_xref="G1:21902030"
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HTG 15-NOV-2002

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                                                                                                                                                                                                                                                                                      Status.

18. Marzy, D. Marzie, Mezzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, M., Alsen, M., Barastead, M., Barastead, M., Barastead, M., Barastead, M., Barastea, M., Carter, M., Cavazoo, M., Carter, M., Cavazoo, M., Carter, M., Cavazoo, M., Chen, Z., Chu, J., Chacko, M., Carter, M., Cavazoo, M., Charaste, M., Carter, M., Cavazoo, M., Delagado, M., Davis, S., Davy, Carroll, M., Chen, Y., Char, M., Charaste, M., Carter, M., Marter, M., Marter
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Direct Submission
Submitted (27-SRP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 222256)
Rat Genome Sequencing Consortium.
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                              Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Nammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
   Rattus norvegicus clone CH230-179K4, *** SEQUENCING IN PROGRESS
                                                                                       AC134482.2 GI:25007228
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                     ***, 2 unordered pieces. AC134482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 222256)
                                                                                                                                                                                        Rattus norvegicus
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DEFINITION
                                                                                                                                                                               ORGANISM
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TITLE
JOURNAL
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REFERENCE
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AUTHORS
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                                                           ACCESSION
                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                         REFERENCE
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Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:23334632. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2737 AACTAGACCCGCTCCTCATCAGTACATTCTCTCTGGGCCTGGACCCTTCTATC 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2677 GITAGCCAGAAGTGAGAACAGGCTCAGGTCCCCTTGTCACACTTCTAAGGGAAGGTCAC 2618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap, version 0.990329
Consensus quality: 190050 bases at least Q40
Consensus quality: 194119 bases at least Q30
Consensus quality: 19564 bases at least Q20
Estimated insert size: 204504; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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    .222256
    /organism="Rattus norvegicus"

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Center clone name: CH230-179K4
-------- Summary Statistics
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/db_xref="taxon:10116"
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Best Local Similarity 53.1'
Matches 69; Conservative
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Library Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON Nov 20, 2002 this sequence version replaced gi:24158508.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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102157. .103191
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48655. .249752
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!46116. .248554
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Best Local Similarity 53.1%;
Matches 69; Conservative
         Direct Submission
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                                                              AC135655 270958 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-6908, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                        AC135655.2 GI:25138854
HTG; HTGS_PHASE1; HTGS_BRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Direct Submission
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                                                                                                                      unordered pieces.
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                                                                                       DEFINITION
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                                                                                                                                                                                                                                             SOURCE
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 248554: contig of 248554 bp in length 1555 248654: gap of unknown length 1865 267829: contig of 19175 bp in length 1863 267829: gap of unknown length 1930 268946: contig of 1017 bp in length 1947 270958: contig of 1812 bp in length 10047 270958: contig of 1912 bp in length.
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Center: Baylor College of Medicine
Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Contact: Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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셤 ò 요 ð 셤

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HDVGLAILGPLRELDLVAYLRFASVYRAFDSLEDFEAAIAELREEQRERPAVDDEDHE
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GFLRRDPHRPRAYEVRGSDQSSSVQPTDTAGKPAASYVPLVGRIAAGGPILAEESVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLKHEHYEVPDCAMGERSISAMGHVRMAAIQPWISGALSKTVNLPETATVEDVEEVY
FEAWKMGVKALAIYRDNCKVGQPLSAKKKETEKAEVTAKTEATIREAVEKVVEYRPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRLPKGRPGITTSFTVGGAEGÝMTANSYPDDGLGEVFLKMSKQGSTLAGMMDAFSIAV
SVGLQYGVPLETYVSKFTNMRFEPAGMTDDPDVRMAQSIVDYIFRRLALDFLPFETRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALGIHSAEERQRHLETGSYEPSDDVDMDVEGLAQSAPRAQELKAVATPKAEVAAAVPA
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                                                                                                   /db_xref="taxon:227882"
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                                                                                                                                                                                                                                                                                                                     /note="SAV2461"
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/gene="lexA"
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gene="lexA"
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                                                     105820 GTTAGCCAGAAGTGAGAACAGGCTCAGGTCCCCCTTGTCACACTTCTAAGGGAAGGTCAC 105879
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Complete genome sequence and comparative analysis of the industrial microcorganism Streptomyces avermitilis
Nat. Biotechnol. 21 (5), 526-531 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                              AP005031 299550 bp DNA linear BCT 10-MAY-2003 Streptomyces avermitilis genomic DNA, complete genome, section
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This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chiqusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7)

Final finishing process and all annotation were done by H. Ikeda and J Ishikawa.
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Submitted (29-MAR-2002) Director-General of Biotechnology Center,
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*2 National Institute of Infectious Diseases
*3 The Kitasato Institute
*4 National Institute of Technology and Evaluation
*5 School of Science, Kitasato University
*6 Institute of Medical Science, University of Tokyo
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Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C.,
Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T.,
Kushida, N., Director-General of Biotechnology Center, Shiba, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M. Genome sequence of an industrial microorganism Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Pollowing url is also available.
http://avermitlis.ls kitasato-u.ac.jp.
Location/Qualifiers
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Streptomyces avermitilis MA-4680
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AP005031.1 GI:29606108
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APSVPARAGATAASADSDGCSDAVDPAAPFAAASTVPSASASRVPSABSADSTATA
APAPAPPSLGDTKALACRQAVSVTRAADDLLGRVEDWGFTVTPAGTFQLAAPTSTATA
PLIGRWNDPRVAAFWKLAGDBSVTRQHLRAQLGGDGRSVPCLGVLEGTPMSYWEITR
PDLSLARHYPARPPAPPTSTHLLIGGVADRGRGLGSTLLRAVADLVLDRRPSCARVVAE
PDLRNTSSVSAFLGAGFRFSAEVDLPDKRAALMVRDRPLRDL"

complement (8549 . 10609)
                      AMLKGRSNYLCLHRILHEGVPQDEEGGLFDQFEAAPTSKIGGDLLRIRDWSDETETGD
TODDLFPGVSDRAWAOVSVSSRECLGATKCAYGAEGFBEWSRERAKLAEVVVTNHALLA
IDAIEGAPVLPQHEVLI VUDEAHELVSKYTGVATGELTPGQNNRAVRRARKLNEKAAD
QLQTPAAEGFERLAMELALPGRILEEI FEDILGYALMALRDAARTVI SAIGATRDKSVQDED
AVRKQALASVESVHDVAER I TNGSEMDVWYERHDRFGASLRVAPMSVSGLLREKLFA
                                                                                                                                                                                                         DRSVVLTSATLKLGGDFNGVGASLGLAPEGTQGDDLPQWKGVDVGSPFDYPKQGILYV
AKHLSRPARDGDRADMLDELTELIQAAGGRTLGFISSWRAAQLAAEELRSRIPEFPIL
LQGEETLGELI KNYBADDFETCLFGTLSLWQGVDVPGPSCQLVVMDXI PFPRPDDPLMS
ARQKAVEDAGGNGFMAVAATHAALLMAQGAGRLVRASGDRGVVAVLDQRLATARYGSY
LKASLPDFWYTTDRNQYRSJLYAIDEAAKKTEVTEVTEVAEVTEEAAKESEGA"
complement (7376. .8509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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QAAAVENLLRCWVRENGLVAPDDGTLRIPLLATGTALLVPVHHWSPTGMHRFGLPYLA
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VYL DORRAPRAPAGEDLI-LAARQALLI-CAPPLAPPKSREGISBRARARI-SPELKGSFR
LHWLAVAPPULATUSPENGSFPVPARQLTARLAGDGLJAMPOGFAALPLHPWOJREIT
RREARAQ-VEHRLLESGGRAPAHPTSSVRTVHRTGAPAMLKLSLGLRITNSRRENL
PREARAALLDAGLIRDLGPHGPAWHPTSSVRTVHRTGAPAMLKLSLGLRITNSRRENL
PREARHROFFREINGSGROWAPHPGPDIVDSPAMLANDGHGNAPFGLDVMIRHN
PRAPTDDVSCVAGLVSRPWPQPTEQPRPWRSRLABIIIRLAGRTGRPRGLVATEWF
LRYLEQVVRPVLMLDSFAGIALEAHQQNTLLLLDPEGWPTGGRYRDNGGYFFRTSRR
RFLADVATGFREINFELDSPVLRCKANLLTRLHGLDELVGFVDDGSVYFRTSRR
RFLADVATGFREINFELDSPVLRCKANLLTRLHGLDELVGFVDTGSVYVTIAN
PLHS.
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/product=10="BAC70178.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVPVRARGLTIEGADGRRYLDCLSGAGTLALGHNHPVVLEAIRKVLDSGAPLHVLDLA
TPVKDAFTTELFRTLPAGLADRARVQFCGPAGTDAVEAAFKLVRTATGRSGLLAFTGA
YHGMTAGALEASGGATDGRVARLPYPQDYRCPFGIGGERGAELGARWTESLLDDVKSG
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YVEBRILDRRAQTIGARALLDQLRSLATEPEPVGBVGRGIMIGVBLYRAEEDRRAVSP
GSGDFASLDTRAGAGRPRAAPELAAAVQRECLRRGLIVELGGRHASVVRLLPPLTISDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="MPPTDASTDAEPATSADPARIAVSARSAADSEDTLELRLPDELV
ALFAAEEAAGGEEAAGGGDGAVRGEEGTAGGEEDAVGGAEFPAGRKDAGPEAQGTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTKASSESSPSASSAGDDKIKIPDDIRDKLKERGIDIDKWKNGAWKNWNRDDWLREAN
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/note="SAV2468"
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/transl_table=
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CDS

CDS

18.2%; Score 32.2; DB 1; Length 299550; 61.2%; Pred. No. 80;

Query Match Best Local Similarity

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PI RADOMIR CREVENJAKOV, MARK DICKSON, SNEZANA GEORGE LAMSON, RADOJE
PI RADOMIR CREVENJAKOV, MARK DICKSON, SNEZANA DRWANAC, IVAN LABAT,
PI DENA LESHKOWITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
PI SIRGIT STACHE CRAIN
PC CLANIS,00, COTRI4,47, CO7K16/18, C12N1/15, C12N1/19, C12N1/21 PC
,C12N5/00,C12Q1/68,
PC CLANIS/00, C12N5/00
CC n = A,T,C or G
FH Key
FT min
                                                                                128986 CCTCCACCGAACCGGACGCGTCGCCCTTGATGATGAGGTTGAGTTCCTGCACCAGACCGG 129045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotza; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases I to 921) Milliams; L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.S., Reinhard,C., Giese,K., Randazzo,F., Kennedy,G.C., Pot,D., Rassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M., and Crain,B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT 17-JUL-2003
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58 CCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              921 bp DNA Human gene and gene expression product V. BD221352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene and gene expression product V Patent: JP 2002534055-A 2465 15-OCT-2002; CHRON CORP, HYSEQ INC OS Homo sapiens (human) PN JP 2002534055-A/2465
                                                                                                                                                                                                                                                     129046 cérrédégecérédrédagairere 129070
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                     118 ACACGAGGCGCCCGTCCCGCTTATC 142
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PF 13-MAY-1999 JP 2000548466
PR 14-MAY-1998 US 60/0854515-MAY-1998 US 60/085696,21-0CT-1998 US 60/105877
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Matches 68; Conserva
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BD221352/c
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VERSION
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JOURNAL
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//note="(RF 7; ptp-2 Op9"
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//product="protein tyrosine phosphatase 2"
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//db_xref="fg1:3749332"
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complement (1. 738)
/note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MAOIKIGOFKEGEDVFTLRYVLDRDIVKFVAKDVASSLKYNICD
KAIRTHVDDKYKTSFEGTIQLGGSTSTNLVKRGDPLYLQPHYVLITKSGVIQLIMKSK
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LQYTQELVKKQEFIERIVATKQYENEBEKALPVLKVWTDLNRWYNGFGETWQKKDEING
QKDAQYTDLVAKVIDLSGRAVQYPEDERKHPVLCVTRDGTTFTALAGQKAYVHNQKLK
RNLSAADIVAEVILYBVYLVDWNNATHRLAAKKSKRTISFDSEQDAQQFATRIKQLLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="wadstrrilrleyprwssktgaslengadlesclydlerfygahmn
kgletsckkkkgaeeraesaalkryelaadrwamgakaapycaddgrwstlsgogled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mosammnpaagysslonsekylidpndfyglalspctvfkogl
Fmemsglrifalltapkptepkravihrskrnvclkacadgsvnlakalnslrmplcm
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EVTHLLIKAEDVYKFSNCAKMYTVNKLCPKAGMCKGKNPICNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tränslation="wasarrikfslryuggfkeniyadithlarlralidgkvthtdv
hrfgfldrnllveacmavnvqvyvpdgtirlnpktiyprvcqkchavadvpapddhsi
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bedsprivwnogewnoyflivinlreyrrengcykflaqharmdcdyvehevirivepsy
vgmneyrislakkggcgptmnihesytnsfesfynkviwenfykpivyigtdsgeee
billevslupkykkefrapapaplefgpay"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MNRPMMRTANAPVIVSNHDYDREQIRRDLNSLRRSVHELCTRST"
AGVNINTTIKPPVPPKPAHLSRPNFMFVGDKVTGNTPPPPNGTSPQPGVNVPPPVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGFDCNRILELSSSSNDVITKSPVIIKNSAATVGQSALVCDKV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="late expression factor 2"
/protein id="AAQ91716.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1247. .1858)
/note="ORF 3; lef-2 Op6/Ac6"
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|db_xref="GI:37499361"
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                                                                                                                                                                                                                                                  /product="polyhedrin"
/protein_id="AAQ91696.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAQ91742.1"
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/note="ORF 4; Op7/Ac5"
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/note="ORF 6; bro Ac2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF 5; Op8/Ac4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(828. .12
/note="ORF 2; Op5"
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/product="unknown"
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FTYKLNRATLLDLLKLAENIYADTAYMQVNTIESSEHFATLAKMRNILLNVQDEHFRN
VLASIVARIENLLRSDAVUNVEITVLSGDFYEEFSRYATRQYVSTDTLPPPPLPPI
PETTQAFVAEPEPPPAQAFVAESPPPAQAFVAESPPPAQAFTARSPGPFFVAPPSBQPT
FVAPSPQATQTPSFRQTFAAPSPVFAESPQPTRAFPTPEGTLSRGAADEFEYRAGTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   July (bases 11500 to 13512)

Barrett, J.W., Krell, P.J. and Arif, B.M.

Characterization, sequencing and phylogeny of the ecdysteroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura funiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The putative LEF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canada On before Oct 8, 2003 this sequence version replaced gi:1117788, gi:2581770, gi:1754838, gi:4092491.

Location/Qualifiers

1. 131158
                                                                                                                                                                          AY327402 131158 bp DNA circular VRL 08-OCT-2003 Choristoneura fumiferana defective nucleopolyhedrovirus complete
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Barrett,J.W., Lauzon,H.A., Mercuri,P.S., Krell,P.J., Sohi,S.S. and
Arif,B.M.
                                                                                                                                                                                                                                                                                                                                         Choristoneura fumiferana defective nucleopolyhedrovirus (CfDEFNPV) Corristoneura fumiferana defective nucleopolyhedrovirus Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lauzon, H.A.M., Jamleson, P.B., Krell, P.J. and Arif, B.M.
Direct Submission
Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry
Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.M. Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 80268 to 81693)
Li,X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and
Arif,B.M.
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/protein_id="AAQ91783.1"
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join[(129349. 131158,1. .20)
/note="0.8F 149; 1629 capeid Op2/Ac9"
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                                                                                                                                                                                                                                                                AY327402 AF068194 U10476 U23422 U78194
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Virus Genes 13 (3), 229-237 (1996)
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Virology 268 (1), 56-67 (2000)
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KEYWORDS
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EINCHAPLETRGASRVQAFFALDSLEFPDNMTDSLQVTMGRRPHFVRGYALTHVANVF
DPTIKLDGWMYNKFCVLTYWRRIIRGTVPAELITRLQNVVTKYIKPEYDESNNALAMG
DPTIKLDGWMYNKFCVLTYWRRIIRGTVPAELITRLQNVVTKYIKPEYDESNNALAMG
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6450. .6723
/note="4 copies of a 30 bp imperfect palindromic sequence;
location similar to Ac hrla"
/function="enhancer; replication origin"
complement (6723. .7871)
                                                                                                                                                                                                                                                        /trānslation="MFPGRWHNYTTCGKVIEGTNLICFKVPLKQEVFEYVTNDEDRWT
VSNLVNRQRALGAVLDLTNTLRYYDGAKVRDAGVLYKKIRVPGQEVPREDIVQEFFDS
VQEPSARCPGMLIGVHCTHGLNRTGYLVCRYIIDKLHVSPTDAIARFEAARGHKIERR
NYLEDLLKRHVRR"
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VYRHDFVKKCVGCRMEVRHDEPTVRONQCALIMWMMTATLDFWNMYVQRKBRRYK
PTPVKTLYFESAPLKEQDTADBEEEQQSSFRMLBIISBPRVOPQFPESSSLDRLSSPP
PIVQSSSSPNSPDSGIDYDIPQPFYSVPNKVVCKYLCRTHATLCA"
PIRQALGLPAGYHIHVYCEDEPTCMALINAMDALYDYIERRINEGKKILIHCHAGVSR
SATLAVYYYMKKWQVSYEKALRFVNNKRNVALSDHFVRFLSSRCTYRFVNNKLKIHVG
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YIESVWRRRHYVPMEALPSVQFDTNLGTLAGETLKCMSVPLYVTEIDLPFFDCTQVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPGASYFFVGEGDTYVVNGHKLAVGGYCTTNSVPRDCNRETSVVLMSLNQWTCIÄEDP
RYFAGTSNMTQLAGRQHFDRILPGQSDRNVLFDRLLGREVNVATNTFRRSWDELLEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRRFEMRCNARDINNNILMFVNPLNPLECLPNVCTNVNYVHTSVRPNFETGECDCGDEA
VTRVRHVVPGDRSSVCASIVDGLDTTTASHRFRVECVNTYTSIGNFSNNKLLCPSDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MLAQINYILQLVLHAALYTITLIAFVFSLMGTINYKYAFLLELN
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Pred. No. 94;
0; Mismatches 5; Indels 0:
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                                                                                                                                                  /codon_start=1
/product="protein_tyrosine_phosphatase_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAA 176
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/note="ORF 11; arif Op19/Ac21"
                                                                                                                     /note="ORF 8; ptp-1 Op10/Ac1"
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/note="ORF 12; Op18/Ac19"
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/db_xref="GI:37499276"
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/db_xref="G1:37499354"
                                                                                                                                                                                                                                                                                                                                                                                                 4935. .5921
/note="ORF 9; Op11/Ac11"
                                                                                            .4676)
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Aca19456 Prokaryot
Ads56860 Bacterial
Abd13439 Pseudomon
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ALIGNMENTS

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| viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral seplication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter. Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2003WO-US022437.  18-JUL-2002; 2003US-0396335P. 26-JUL-2002; 2003US-0427231P. 24-WAR-2002; 2003US-0427231P. 24-WAR-2003; 2003US-0474940P.  (INVI-) INVITROGEN CORP. (BENN/) BENNETT R P. (WELC/) WELCH P J. (HARW) HARWOOD S. (MADD/) MADDEN K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more   | viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral seplication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter. Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2003US-0396335P. 26-JUL-2002; 2003US-0396335P. 26-JUL-2002; 2003US-0427231P. 24-WAR-2003; 2003US-0427231P. 24-WAR-2003; 2003US-0474940P.  (INVI.) INVITROGEN CORP. (BENN/) BENNETT R P. (HARW/) HARWOOD S. (MADD/) MADDEN K. (FRIM/) FRIMPONG K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more  | viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral seplication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter. Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2003; 2003WO-US022437.  18-JUL-2002; 2002US-0398617P.  19-NOV-2002; 2002US-0427231P.  24-WAR-2003; 2003US-0427231P.  24-WAR-2003; 2003US-045446P.  (INVI-) INVITROGEN CORP. (BENN/) BENNETT R P. (WELC/) WELCHP J. (HARW/) HARWOOD S. (MADD/) MADDEN K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more   | viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral seplication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter. Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2002US-0396335P. 26-JUL-2002; 2002US-0398617P. 19-NOV-2002; 2002US-0427231P. 24-MAZ-2003; 2003US-0427231P. 24-MAZ-2003; 2003US-0456496P. 03-JUN-2003; 2002US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2002US-042731P. 03-JUN- |
| viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral vector; despeneration; gene deneration-defective particle generation; gene gene therapy vector; de; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2003US-0386335P. 26-JUL-2002; 2003US-038637P. 19-NOY-2002; 2003US-0427231P. 24-WAR-2003; 2003US-047781P. 24-WAR-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. (INVI.) INVITROGEN CORP. (BENN/) BENNETT R P. (HARW/) HARWOOD S. (MADDEN K. (FRIM/) FRIMPONG K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more  | viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral vector; despeneration; gene deneration-defective particle generation; gene gene therapy vector; de; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2003US-0396335P. 26-JUL-2002; 2003US-0396335P. 26-JUL-2002; 2003US-0398617P. 19-NOY-2002; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0456496P. 03-JUN-2003; 2003US-0474940P. (WELCY) WELCH P J. (HARW/) BENNETT R P. (HARW/) HARWOOD S. (MADD) MADDEN K. (FRIM) FRIMPONG K. (FRIM) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more  | viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral vector; despeneration; gene deneration-defective particle generation; gene gene therapy vector; de; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2003US-0396335P. 26-JUL-2002; 2003US-039637P.  19-NOV-2002; 2003US-0427231P. 24-WAR-2003; 2003US-0474940P.  (INVI-) INVITROGEN CORP. (BENN/) BENNETT R P. (WELC/) WELCH P J. (HARWO) S. (MADD/) MADDEN K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more   | viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral vector; despeneration; gene deneration-defective particle generation; gene gene therapy vector; de; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2002US-0396335P. 26-JUL-2002; 2002US-0396315P. 26-JUL-2002; 2002US-0427231P. 24-MAR-2003; 2003US-0427231P. 24-MAR-2003; 2003US-045496P.  (INVI) INVITROGEN CORP. (BENN/) BENNETT R P. (WELC/) WELCH P. (HARW/) HARWOD S. (HARW/) HARWOD S. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more  |
| viral vector; recombination site; recombinant viral vector; recombination site; recombination replication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2002US-0396335P. 26-JUL-2002; 2002US-0396617P. 19-NOY-2002; 2003US-0456496P. 24-MAR-2003; 2003US-0456496P. 33-JUN-2003; 2003US-0456496P. 33-JUN-2003; 2003US-0456496P. 34-MAR-2003; 2003US-0456496P. 35-JUN-2003; 2003US-0456496P. 36-JUN-2003; 2003US-0474940P.  (INVI.) INVITROGEN CORP. (RELN/) BENNETT R P. (HARW/) HARWOOD S. (MADD) MADDEN K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more  | viral vector; recombination site; recombinant viral vector; recombination site; recombination replication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2002US-0396335P. 26-JUL-2002; 2002US-0396617P. 19-NOV-2002; 2003US-0456496P. 24-MAR-2003; 2003US-0456496P. 33-JUN-2003; 2003US-0456496P. 33-JUN-2003; 2003US-0456496P. 34-MAR-2009; 2003US-0456496P. 35-MADDEN R. (RELN/) RENNETT R P. (HARW/) HARWOOD S. (MADD) MADDEN K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more   | viral vector; recombination site; recombinant viral vector; recombination site; recombination replication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2002US-0396335P. 26-JUL-2002; 2002US-039637P. 19-NOY-2002; 2002US-039617P. 19-NOY-2002; 2003US-0456496P. 03-JUN-2003; 2003US-0474940P.  (WELC/) WELCH P J. (HARW/) HARWOOG S. (MADDEN K. (FRIM/) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more   | viral vector; recombination site; recombinant viral vector; recombination site; recombinant viral replication-defective particle generation; gene gene therapy vector; ds; OpIE2 promoter.  Unidentified.  WO2004009768-A2.  29-JAN-2004.  18-JUL-2002; 2002US-0396335P. 26-JUL-2002; 2002US-0396335P. 26-JUL-2002; 2002US-0427231P. 24-WAR-2003; 2003US-0474940P.  (INVI-) INVITROGEN CORP. (BENN/) BENNETT R P. (WELC/) WELCHP J. (HARWOD S. (HARW) HARWOD S. (HARW) HARWOD S. (HARW) HARWOD S. (HARW) FRANKE K E.  Bennett RP, Welch PJ, Harwood S, Madden K, F WPI; 2004-132944/13.  Novel nucleic acid molecule comprising all or a viral genome and further comprising two or more   |

AAS61341 ADF83430

3107 3501 6107 6107 6107

113

3448 3600 29169 1404 657

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portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 474
                                                                                                                                                                                                               recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpiE2 promoter that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene
                                                       invention comprises a nucleic acid molecule consisting of all or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 CGAGGGCCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTCTTATCGTGACACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 GICTIATCGICACAGGACGCCAGCTICCIGIGITGCTAACCGCAGCCGGACGCAACTCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pseudotsugata multicapsid nucleopolyhedrosis virus ie2 promoter.
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0
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 177; DB 12; Length 560; 100.0%; Pred. No. 2.6e-48; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                             Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orgyja pseudotsugata; polyhedrosis virus
                Disclosure; Fig 16; 555pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ion transport peptide hormone; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYBR-) UNIV BRITISH COLUMBIA.
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98CA-02221819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV62487 standard; DNA; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Matches 177; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1997;
28-JAN-1998;
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19-JAN-1999
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that comprises: (i) prokaryotic origin of replication; (ii) insect that comprises: (i) prokaryotic origin of replication; (ii) insect carly baculovirus promoter; (ii) prokaryotic promoter aguence, and (iv) carly baculovirus promoter; (iii) prokaryotic promoter aguence, and (iv) calctable marker capable of conferring resistance to a bleomycin/ promoter; (iii) in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologus DNA, useful to allow study of gene expression and direct expression of heterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell insect cells modification of particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be curther comprising DNA transposable elements defining a transposon can be considered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TATCGGAACAGGACGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 TATCGGAACAGGGGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to optimise Meterologous protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multimeric protein; interleukin 5; ILS; TNFalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471 CGAGGGCCCCGTCCCGCTTATCGCCCCTATAAATACAGCCCGCAACGATCTGGTAAA 527
                                                                                     This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis virus (OpMNPV) immediate early 2 (Op le2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells that comprises: (1) prokaryotic origin of replication; (ii) insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCGGACGCAACTCCT
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 564 BP; 147 A; 160 C; 116 G; 141 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
expression and produce commercially important proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                              Claim 10; Page 82; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2002; 2002WO-DK000764.
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16-NOV-2001; 2001US-0331575P.
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Best Local Similarity 100.
Matches 177; Conservative
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(FRIM/) FRIMPONG K. (FRAN/) FRANKE K E.
                                                                                                                                                                                                                                                                                                                              Similarity
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26-JUL-2002;
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24-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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                              Bennett RP,
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                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                         The invention relates to immunogenic analogues of multimeric proteins ench as immunogenic variants of interleukin 5 (ILE) and tumour necrosis factor alpha (TNF, TNFalpha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in gene therapy. The present sequence is p220p2F expression vector for insect cells. This sequence is p220p2F expression vector for
                                                                                                                                                                                                                                                                                                                               TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                         355 GICTIATCGIGACAGGACGCCAGCTICCIGITIGCIAACCGCAGCCGGACGCAACICCI 414
                                                                                                                                                                                                                                                                                                                                                    415 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGGGTGACCGGACA 474
                                                                        preparing a
                                                                                                                                                                                                                                                                                                                                                                       CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                   replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid.
                                                                                                                                                                                                                                                                                     1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                .
0
                                                                      New immunogenic analogue of a polymeric protein, useful for por
composition for treating inflammatory diseases e.g. arthritis
                                                                                                                                                                                                                                           Length 2773;
                              Mouritsen S;
                                                                                                                                                                                                                       Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viral vector; recombination site; recombinant virus;
                                                                                                                                                                                                                                           100.0%; Score 177; DB 9; 100.0%; Pred. No. 3.8e-48;
                             Voldborg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral vector-related plasmid - pIB/V5-His-DEST
                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                      Disclosure; Page 195-196; 196pp; English.
                              Bratt T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ48539 standard; DNA; 5038 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002US-0396335P.
2002US-0398617P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-NOV-2002; 2002US-0427231P-24-MAR-2003; 2003US-0456496P-03-JUN-2003; 2003US-0474940P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2003; 2003WO-US022437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 177, Conservative
                             Nielsen FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVITROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BENNETT R P.
WELCH P J.
HARWOOD S.
         MOURITSEN S
                                                 WPI; 2003-449558/42
VOLDBORG B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MADDEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004009768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004
                              Klysner S,
                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ48539,
                                                                                                                                                                                                                                           Query Match
        (MOUR/)
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(WELC/)
(HARW/)
(MADD/)
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portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombining each other. One or more of the recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The mucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a nlasmid that more construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           351 Grerraregradadadececaderrecrererracraacededeceadecedadecea 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCACGTGACCGGACA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TATCGGAACAGGACGCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                 that
                                                                                                                                             Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replication-defective particle generation, gene expression inhibition, gene therapy vector, ds, plasmid, recombination region.
Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTAGCCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viral vector-related plasmid pIB/V5-His-DEST recombination region #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 5038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
   Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 175.4; DB 12; Lucy Pred. No. 1.5e-47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral vector; recombination site; recombinant virus;
   Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                       Example 18; Page 395-403; 555pp; English.
   Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0396335P.
2002US-0398617P.
2002US-0427231P.
2003US-0456496P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2003; 2003WO-US022437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 176; Conservative
   Welch PJ,
                                                                          WPI; 2004-132944/13
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(WELC/) (HARW/) (MADD/) (MADD/) (FRIM/)

INVI-BENN/)

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76 CGCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                libraries constructed from human colon cancer cell lines. The present libraries constructed from human colon cancer cell lines. The present convention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                             Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 decagérdecenceagérdecreréceacécedrerécecececécérdecedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 7876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 921 BP; 239 A; 214 C; 205 G; 223 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.1%; Score 32; DB 3; Length 921; llarity 51.5%; Pred. No. 2.1; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 989; 1097pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL18801 standard; DNA; 1268 BP.
98US-0105877P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 TAAGATCGNGCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                          Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                        Escobedo
                                                                                                                                                                                                                                                 WPI; 2000-126369/11.
                                                (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 68; Conserv
                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200171042-A2
  27-OCT-1998;
                                                                                                                        Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL18801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product; probe;
breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises a nucleic acid molecule consisting of all or a
                                                                                                                                                                                                                                                   Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon cancer cell line polynucleotide sequence SEQ ID NO:2465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 23.2%; Score 41; DB 12; Length 141; I Similarity 100.0%; Pred. No. 0.0014; 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   Madden K, Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; tumour; diagnosis; gene expression pri
detection; cancerous state; metastasis; identification; bri
oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 41
                                                                                                                                                                                                                                                 Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 17; 555pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA02474 standard; cDNA; 921 BP
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98US-0085537P.
98US-0085696P.
98US-0105234P.
  03-JUN-2003; 2003US-0474940P.
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                                                   INVITROGEN CORP.
                                                                                                                                                                                                                                                   Welch PJ,
                                                                       BENNETT R P. WELCH P J. HARWOOD S.
                                                                                                                                                                                                                                                                                                  WPI; 2004-132944/13.
                                                                                                                                               MADDEN K.
FRIMPONG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                   (FRAN/) FRANKE K E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9958675-A2
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                                                                                                                                                                                                                                                      Bennett RP,
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RESULT 6 AAA02474/c

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ABL27502;
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                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), processed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                           657 Acaacaderricegargaagargeeceacaageggereeragieeriegeeggeereee 716
                                                                                                                                                                                                                                                                                                                                                                                                                                     9/
                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 33982.
                                                                                                                                                                                                                                                                                                                                                                                  Score 30.8; DB 4; Length 1268;
Pred. No. 5.6;
0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                          Sequence 1268 BP; 295 A; 336 C; 360 G; 277 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 GCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 762
                                                                                                                                                                                          Claim 1; SEQ ID NO 7876; 21pp + Sequence Listing; English
                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
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                                                                                      PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL27503 standard; DNA; 1342
 23-MAR-2001; 2001WO-US009231
                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                   17.4%;
ilarity 55.7%;
Conservative
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                                                                                      Adams M,
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                                                                                                               WPI; 2001-656860/75
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                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                interactions
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 59
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                                                                                      Venter
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ABL27503
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7177). ABBS72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             731 ACAACAGCTTCCGGTGGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genomic polynucleotide SEQ ID NO 33979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30.8; DB 4; Length 1342; Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1342 BP; 324 A; 347 C; 372 G; 299 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            791 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 836
                                                                                             Claim 1; SEQ ID NO 33982; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.7%;
Matches 59; Conservative
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                                               interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7737-ABB772072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                             17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 7873.
                                                                                                                                                  Score 30.8; DB 4; Length 3448; Pred. No. 7.1; 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                              1607 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
                                                                                                                                                                                                                                                                                                        77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                Sequence 3448 BP; 894 A; 817 C; 801 G; 936 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3600 BP; 946 A; 856 C; 823 G; 975 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 7873; 21pp + Sequence Listing; English.
                                                                           from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ABL18800 standard; DNA; 3600 BP.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                          59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; gene;
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                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding
                                                                                                                                                                                                                                                                                        Carcinoma-associated protein; CAP; acinar cell carcinoma; fibrosarcoma;
Kaposi's sarcoma; breast cancer; Hairy cell leukaemia; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TBX21 protein, useful for screening a bloactive agent capable of bir to carcinoma associated protein, and for evaluating the effect of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29169 BP; 5725 A; 7553 C; 7224 G; 8641 T; 0 U; 26 Other;
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0
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                                                                                        GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
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                                                            GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant carcinoma-associated protein such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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Mismatches
                                                                                                                                                                                                                                                           (CA) gene TBX21.
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 4; Opp; English.
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                                                                                                                                                                   AAD64735 standard; DNA; 29169
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02-MAR-2001; 2001US-00798586.
08-NOV-2001; 2001US-00052482.
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61.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2002; 2002US-00105613.
                                                                                                                                                                                                                                                             Human carcinoma-associated
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         candidate carcinoma drug.
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                                                                                                                                                                                                                                                                                                                                                                 US2003099963-A1
                                                                                                                                                                                                                               11-MAR-2004
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AAD64735
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Gaps

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Score 30.8; DB 4; Length 3600; Pred. No. 7.2; 0; Mismatches 47; Indels 0;

ch 17.4%; 1 Similarity 55.7%; 59; Conservative

Query Match Best Local Similarity Matches 59; Conserv

Length 1404;

DB 13;

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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; heat tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; introgen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
                                                                                                                                                                                                                                                                                                 Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 45503; 122pp; English.
                                                                                                                                                                                                                                                                                                Chen X,
                ADT47065 standard; cDNA; 1404 BP
                                                                   Bacterial polynucleotide #21816.
                                                                                                                                                                                                                                                                                                Cao Y, Hinkle GJ, Slater SC,
                                                                                                                                                                                                            20-FEB-2003; 2003US-00369493
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                                                  (first entry)
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HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                               GOLDMAN B S.
                                                                                                                                                                        US2003233675-A1.
                                                  02-DEC-2004
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                                 ADT47065;
                                                                                                                                                        Bactería.
                                                                                                                                                                                                                                                                               (GOLD/)
                                                                                                                                                                                                                                             CAOY/)
                                                                                                                                                                                                                                                             (SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                      (HINK/)
RESULT 12
        ADT47065
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant accompinant DNA construct and opposity. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the recombinant DNA construct and growing the transformed plant where the polymucleotide or polypeptide is useful for improved plant properties, e.g. improved cold, heat or drought tolerance, confirmant DNA construct is useful for producing plants with the recombinant DNA construct is useful for improved plant, where the polymucleotides, extreme osmotic conditions, pathogens or tolerance to herbicides, extreme osmotic conditions, pathogens or tolerance to be plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or production, improved lighin production or improved algain production or improved algain production or improved algain production or improved dignin production New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Sequence 1404 BP; 236 A; 489 C; 454 G; 225 T; 0 U; 0 Other;

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                                                          99 ATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCCTATAAATACAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a polynucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression
                                                                               464 ACCGCAAGGCGTGAACGTGCCCGATGTGGTGCTGCCGCCTTGCCGCCTTTCGGCCAAGG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with isoprenoid
its, for targeted
                                                                                                                                                                                                                                                                                                                                 isoprenoid biosynthesis; ss; isopentenyl diphosphate; IPP; dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotides and polypeptides associated with iso synthesis in plants, useful for producing transgenic plants, for gene disruption, as well as markers or probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ghassemian M, Briggs SP, Cooper B, Glazebrook J;
(atagiri F, Kreps J, Moughamer T, Provart N, Ricke
                               ö
                               Indels
                             29;
                                                                                                                                                                                                                                                                                                      Plant isoprenoid biosynthesis-associated DNA #6.
Score 30.6; DB
Pred. No. 6.7;
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 563; 117pp; English
                                                                                                                                                                                                                     ВЪ
                                                                                                                 159 CCCGCAACGATCTGGTA 175
                                                                                                                                            524 Acceceáceárcrecaa 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2001; 2001US-0325277P.
04-APR-2002; 2002US-0370620P.
04-APR-2002; 2002US-0370743P.
 Query Match 17.3%;
Best Local Similarity 62.3%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2002; 2002US-00259194
                                                                                                                                                                                                                     ADI45632 standard; DNA; 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRIGGS S P.
COOPER B.
GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LANGE B M.
GHASSEMIAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KREPS J.
MOUGHAMER T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-090562/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROVART N. RICKE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOFF S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004010815-A1
                                                                                                                                                                                                                                                                                                                                                                                                           haeme; yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                           22-APR-2004
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Goff SA,
                                                                                                                                                                                                                                                ADI45632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LANG/)
(GHAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KATA/)
(KREP/)
(MOUG/)
(PROV/)
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(GOFF/)
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cassette. The polypeptides and polynucleotides include those associated with the biosynthesis of isopenic plant comprising the expression cassette. The polypeptides and polynucleotides include those associated with the biosynthesis of isopencenyl diphosphate (IPP) and dimethylallyl alcohol (DMAPP), the biosynthesis of short-chain plastid properties of carotenoids and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phylloquinone biosynthesis of tocopherols, phytosterol and brassinosteroid metabolism, biosynthesis of ubiquinone, phytosterol and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polynucleotides. The polynucleotides are useful for producing transgenic plants, where the genome is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a corresponding gene has been disrupted, e.g. to result in a corresponding product than the corresponding wild-type plant. The better quality product than the corresponding wild-type plant. The corresponding are useful for targeted gene disruption, as well as markers and probes: Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at 1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 TGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                             segdata.uspto.gov/sequence.html?DocID=20040010815. The present sequence is an isoprenoid biosynthesis- associated DNA included in the sequence listing but not mentioned anywhere else in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 GCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 GCCGCATGATTGCGTGTTCTCGTGCCGGGTCTCGACGGGGCCGGCTGGCCTCCCGCGC 389
cassette comprising the polynucleotide, a host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 16.9%; Score 30; DB 12; Length 657; I Similarity 53.4%; Pred. No. 8.9; 63; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 657 BP; 109 A; 257 C; 178 G; 113 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABD14088 standard; DNA; 1710 BP
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P-PSDB; ABO80517.
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Best Local Similarity
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27-JUL-1998;
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Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for autibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-ABD17967 represent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
useful as molecular targets for diagnostics, prophylaxis and treatment of
pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 CCATATCAGCCGCGCGCTTATCTCATGCGCGTGACCGGACACGAGGGCGCCCGGTCCCGCTTA 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; cell proliferative disorder; breast; methylation; cytostatic; gene therapy; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 11; Length 1710;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1710 BP; 380 A; 455 C; 526 G; 349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Indels
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Look MP,
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Schmitt M,
                                                                                                 Disclosure; SEQ ID NO 12692; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS89385 standard; DNA; 3107 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seqdata.uspto.gov/sequence.html
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07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.9%;
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Best Local Similarity 57.4
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rujan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-348468/32.
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Nimmrich I,
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ADS89385/c
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Search completed: May 10, 2005, 04:32:48 Job time : 201.559 secs This Page Blank luspiol

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Sequence 12692, A Sequence 2371, Ap Sequence 11301, Ap Sequence 12333, A Sequence 12233, A Sequence 22, Appl Sequence 22, Appl Sequence 5, Appl Sequence 5, Appl Sequence 1399, Ap Sequence 7217, Ap Sequence 7217, Ap Sequence 11824, A Sequence 13193, A Sequence 2740, Ap Sequence 2763, Ap
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Sequence
Sequence
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-902-540-2311
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US-09-252-991A-12370
US-09-252-991A-12323
US-09-252-991A-12323
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US-09-902-540-1233
US-09-902-540-12193
US-09-902-540-12193
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177
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match Length
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|---|---|---|---|---|
| 1377 4 US-09-222-991A-14970<br>1377 4 US-09-502-540-244<br>1524 4 US-09-002-540-2099<br>4194 4 US-09-002-540-2099<br>4902 4 US-09-902-540-318<br>9080 4 US-09-902-540-1963<br>12865 4 US-09-902-540-1164<br>15209 4 US-09-902-540-1164<br>15351 4 US-09-902-540-1154<br>16925 4 US-09-902-540-1154<br>15351 4 US-09-002-540-1154<br>16926 4 US-09-252-991A-20<br>1182 4 US-09-252-991A-193<br>1701 4 US-09-252-991A-219<br>1938 4 US-09-252-991A-22<br>1938 4 US-09-252-991A-22<br>1938 4 US-09-252-991A-22<br>20093 4 US-09-252-991A-22<br>17772 4 US-09-49-016-17417  | MINO ACID<br>GNOSTICS P<br>91A<br>8   | 16.9%; Score 30; DB 4; Leng imilarity 57.4%; Pred: No. 2; Conservative 0; Mismatches 40; I. CCATATCAGCGCGCGGAGACGGGGGGGGGGGGGGGGGGG | CCAAAATAGCCGCTCGATCTCTCGGCGAAGTGACGGGGCACCTGGCGAGCGCATTGCCCC<br>TCGCGCCTATAAATACAGCCGCAACGATCTGGT 174<br> | 09-902-540-2371 equence 2371, Application US/09902540 atent No. 6833447 ENERAL INFORMATION: APPLICANT: Goldman Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Miegand, Roger C. APPLICANT: Wiegand, Roger C. TITLE OF INVENTION: Myxococcus xanthus Genome Sequences FILE REFERENCE: 38-10(15849)8 FILE REFERENCE: 38-10(15849)8 CURRENT FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: 60/217,883                                  |
| C 298 27.2 15.4 23.3 27.2 15.4 4.4 2.7 2 15.3 4.4 2.7 2 15.3 4.4 4.5 27.2 15.3 2.7 2 15.3 2 2.7 2 15.3 2 2 2.7 2 15.3 2 2 2 2 15.2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2  | RESULT 1  US-09-252-991A-12692/C  Sequence 12692, Application US/09252991A  Sequence 12692, Application US/09252991A  Patent No. 6551795  GENERAL INFORMATION: APPLICANT: MARC 10. TITLE OF INVENTION: NUCLEIC ACID AND AND TITLE OF INVENTION: NUCLEIC ACID AND AND TITLE OF INVENTION: ARRUGINOSA FOR DIANCE TITLE OF INVENTION: ARRUGINOSA FOR DIANCE TITLE OF INVENTION: ABRUGINOSA FOR DIANCE TITLE OF INVENTION: ARRUGINOSA FOR DIANCE TITLE OF INVENTION: ARRUGINOSA FOR DIANCE APPLICATION NUMBER: US 60/074,78  PRIOR FILING DATE: 1998-02-18  PRIOR FILING DATE: 1998-02-18  PRIOR FILING DATE: 1998-07-27  NUMBER OF SEQ ID NOS: 33142  SEQ ID NO 12692  LENGTH: 1110  TYPE: DNA  ORGANISM: PSEUGGONORAE aeruginosa US-09-252-991A-12692 | Query Match<br>Best Local S<br>Matches 54   | Db 414 CCAAAATAGC Qy 141 TCGCGCCTAT Db 354 TCGCCCGTC  | RESULT 2 US-902-540-2371 Sequence 2371, Application US/09902540 Patent No. 683347 GENERAL INFORMATION: APPLICANT: HINKLE, Gregory J. APPLICANT: HINKLE, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Slater, Steven C. TITLE OF INVENTION: Wyxococcus xanthu FILE REFERENCE: 38-10(15849)B CURRENT APPLICATION NUMBER: US/09/902 CURRENT FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10 |

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Sequence 12370, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT:
MATCJ INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION WOMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-02-18
PRIOR PILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry J.

APPLICANT: Glater, Steven C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wie
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Pred. No. 4.3;
0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                Score 29.8; DB 4; Length 1311; Pred. No. 2.1; 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 TGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTA 149
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Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                    ; TYPE: DNA; ORGANISM: Myxococcus xanthus US-09-902-540-2371
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NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2371
LENGTH: 1311
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Parent No. 655173.

Ratent No. 655173.

Ratent No. 655173.

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFREENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12323

LENGTH: 1551
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12097
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                                                                                                                                                                                                                       Length 585;
                                                                                                                                                                                                                                                                                                                                               54; Indels
                                                                                                                                                                                                                             DB 4;
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16.2%; Score 28.6; DB
Best Local Similarity 53.0%; Pred. No. 4.3;
Matches 61; Conservative 0; Mismatches
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Patent No. 6551795
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-12323/c
                                                                       ; UKGANTON: .....
US-09-252-991A-12370
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55 ACTCCTTATCGGAACAGGGCGCCTCCATATCAGCCGCGCGTTATCTCTCATGCGCGTGAC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507 cgggchccgggrgcccarccgggcchgcccgcgcrccaccacacacacagaacacrgcgg 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.2%; Score 28.6; DB 3; Length 2091; 58.0%; Pred. No. 6.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENTARE: MITERALM GENERALCOMMORER: US/09/126,121
PILING DATE: 30-Jul-1998
CLASSIFICATION:
RICHARD NOTE: 30-Jul-1998
CLASSIFICATION:
NAME: CONING DETAINS:
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 91084R1D1
TELECOMMUNICATION NUMBER: 650/25-2066
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P1084R1D1
                                                                                              P1084R1
                                                                                                                                                                                                                                                                                                                                                                   Human NRG3B2 (hNRGB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09126121
Patent No. 6252051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WinPatin (Genentech)
                                        NAME: Conley, Deirdre L. REGISTRATION NUMBER: 36,487 REFERENCE/DOCKET NUMBER: P10 TELECOMMUNICATION INFORMATION: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc. STREEF: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 2091 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2091 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94080
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US-09-126-121-22
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                                                                                                                                                                                                                                                                                                                                            FEATURE:
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Sequence 12237, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

HURORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12237

LENGTH: 2085
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                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CGTGACAGGACGCCAGCTTCCTGTGTTACCAAGCCGGACGCAACTCCTTATCGGA 67
                                                                                                                  8 CGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGA
                                                                                                                                                                                                                 68 ACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                     655 GCTGGACGCGCGCAGATCAAGCCGCAGGTCAGCTGGGCACGTCGCCGGAAATG 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 ACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          862 GCTGGACGCCGCGCAGATCAAGCCGCAGGTCAGCTGGGGCACGTCGCCGGAAATG 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                      Length 1551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Score 28.6; DB 4; Length 2085; 53.0%; Pred. No. 6.3;
                                                                    54; Indels
                    Score 28.6; DB 4;
Pred. No. 5.8;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                 ch 16.2%;
1 Similarity 53.0%;
61; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.0
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-12237
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                                                                  Matches
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us-09-896-888a-1\_copy\_351\_527.rni

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Linear
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Best Local Similarity
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US-09-902-540-1239
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FEATURE:
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                                                                                           RESULT 11
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                                                                                                                                                                                                                                                                     448 ACGCCCAACCGGATTAGCACTCGCCTGACCA-TCACGCGGGGGCGCCCACTCGCTTCCC 506
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                                                                                                                                                                                                                                                                                                                 115 CGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGG 173
                                                                                                                                                                                                                                                                                                                                                              115 CGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGG 173
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                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor
                                                                                                                                 Score 28.6; DB 3; Length 2091; Pred. No. 6.3; 0; Mismatches 49; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Score 28.6; DB 3; Length 2502; ilarity 58.0%; Pred. No. 6.7; Conservative 0; Mismatches 49; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Human NRG3B1 (hNRG3B1) /nucleic acid seg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Winbatin (Generical)
SOFTWARE: Winbatin (Generical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Uul-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidic L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 19,487
TELEPHONE: 650/225-2066
Human NRG3B2 (hNRGB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-899-437-5; Sequence 5, Application US/08899437; Patent No. 6121415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9811
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2502 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                 Query Match
Best Local Similarity 58.0%;
Matches 69; Conservative
                  LOCATION: 1-2091
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD: OTHER INFORMATION: .
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Best Local Similarity
Matches 69; Conserv
NAME/KEY:
                                                                      ;
US-09-126-121-22
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650 CGGGCACCGGGTGCCCATCCGGGCCAGCCGCGCTCCACCACAGCACGGAACACTGCGG 708
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Patent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Steven C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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Pred. No. 6.7;
0; Mismatches 49; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 30-Jul-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P1084R1D1
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NAME: Conley, Deirdre L.
REGISTRATION UNDRER: 36,487
REFERENCE/DOCKET UNDRER: P1084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-2066
TELEPHONE: 650/252-2086
TEMPER NUCLEIC ACID
STRANDENESS: Single
                                                                                                                                                                                                                                          US-09-126-121-5
; Sequence 5, Application US/09126121
; Patent No. 6252051
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1 Similarity 58.0%;
69; Conservative 0
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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RESULT 14
US-09-513-999C-27806
; Sequence 27806, Apl
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Fatent No. 6812339
GENERAL INFORMATION;
FATENCE INFORMATION;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR PELLOR TON NUMBER: 60/231,498
FRIOR PRILING DATE: 2000-10-03
FRIOR PELLOR DATE: 2000-10-03
FRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRATSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6260 TTTTTTTGACGACACTCCACCCATCGATGTTGGTACCAGGGGGTGGAAACATCGAAATCA 6319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6320 dérrcardaagrrccccagaagcaadccrradcaaccrcacarrodaaarcercaacer 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 GCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTAT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 GGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
16.2%; Score 28.6; D:
Best Local Similarity 49.0%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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49.3%; Pred. No. 20;
CURRENT APPLICATION NUMBER: US/09/902,540
                                   CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1239

LENGTH: 25048

TYPE: DNA

ORGANISM: Myxococcus xanthus

US-09-902-540-1239
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LOCATION: (1)...(57320)
OTHER INFORMATION: n = A,T,C or G
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Matches 74; Conservative
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LENGTH: 57320
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                                                                                                                            FACELIANT: DUAGENTION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT FILING DATE: 1990-02-24.
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PRILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 27806
LENGTH: 283
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: WINGER STEVEN C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Steven C.
APPLICANT: Wi
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Pred. No. 9.6;
0; Mismatches
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Best Local Similarity 68.4%; Pred. No. 4.8;
Matches 39; Conservative 0; Mismatches
Caywence 27806, Application US/09513999C Patent No. 6783961
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 7217
LENGTH: 2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: v=a or c or g
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Best Local Similarity 54.3%;
Matches 57; Conservative
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ORGANISM: Myxococcus xanthus
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NAME/KEY: misc_feature
LOCATION: 197
OTHER INFORMATION: k=g or
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NAME/KEY: misc_feature
LOCATION: 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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- 1657 CAGGTGACGGGCTTCGCGGGTTGCTCCAGCCCAAACGCCGGAAGCCAGGGGGAGTAC 1716

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q à Search completed: May 10, 2005, 07:29:35 Job time : 60.8508 secs

Sequence 50761, A
Sequence 35867, A
Sequence 44133, A
Sequence 65984, A
Sequence 22976, Ap
Sequence 7126, Ap
Sequence 7126, Ap
Sequence 22, App1
Sequence 22, App1

Sequence 563, App Sequence 303, App Sequence 10, Appl Sequence 4094, Ap Sequence 72869, A

Sequence :

Sequence 22, Appl Sequence 22, Appl Sequence 22, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 41603, A Sequence 33339, A Sequence 33339, A

Sequence 176225, Sequence 40821, A Sequence 58, Appl Sequence 166, App Sequence 135441,

Sequence

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Gaps

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Score

Result g 175.4

309

9

Perfect score:

Sequence:

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Run on:

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61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 177; DB 9; Length 462; 100.0%; Pred. No. 1.5e-54; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-136-5734-5
US-10-136-5734-5
US-10-215-862-5
US-10-369-493-41603
US-10-282-122A-33339
US-10-425-114-17146
US-10-425-115-176225
US-10-425-115-40821
US-10-034-650-58
US-10-034-650-58
US-10-034-650-58
US-10-037-650-115-40821
US-10-037-650-115-40821
US-10-037-650-58
US-10-037-650-118-4
8 US-10-437-963-42126

8 US-10-437-963-52473

US-10-221-613-303

7 US-10-221-613-303

7 US-10-221-613-303

7 US-10-275-311A-10

8 US-10-437-963-72869

8 US-10-437-963-72869

8 US-10-437-963-72869

8 US-10-437-963-35867

7 US-10-369-493-44133

8 US-10-425-4072

US-10-029-386-22976

US-10-029-386-22976

US-10-029-386-22976

US-10-029-386-22976

US-10-029-386-22976

US-10-029-386-22976

US-10-029-386-22976

US-10-369-493-32534

US-10-369-493-32534

US-09-817-667-22

US-10-369-493-32534

US-10-215-862-22

US-10-215-862-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Insect Expression Vectors
TITLE OF INVENTION: Insect Expression Vectors
FILE REPERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-817-647-5
US-09-877-665-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09896888A Patent No. US20020116723A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 177; Conservative
                                              1320
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2019
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29322
75839
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1623
    US-09-896-888A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Sequence 1, Appli
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2164.037 Million cell updates/sec
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Sequence 60,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     '(gn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US06_Brime PUB.seq:*
'(gn2_6/ptodata/1/pubpna/US06_Brime PUB.seq:*
'(gn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
'(gn2_6/ptodata/1/pubpna/US08_BrimeOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:*
'(gn2_6/ptodata/1/pubna/US10B
                                                                                                                                                 May 10, 2005, 05:52:55 ; Search time 500.12 Seconds
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-295-074-60
US-10-846-911-60
US-10-622-088-89
US-10-622-088-127
US-10-622-088-127
US-10-156-761-2538
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US-10-369-493-45503
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US-10-622-088-126
US-09-896-888A-1
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                                                                                                                                                                                                                                                                                                                                                                                 5654200 seqs, 3057283753 residues
                                                                                                                                                                                                                                    US-09-896-888A-1_COPY_351_527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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32.2
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PRIOR FILING DATE: 1998-03-26
PRIOR PELLING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
LENGTH: 564
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ORGANISM: Artificial sequence
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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Best Local Similarity 100.(
Matches 177; Conservative
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LOCATION: (625)..(630)
OTHER INFORMATION: Clai
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310 TATCGGAACACGCGCCCCCCCATATCAGCCGCGCGTTATCTCTATGCGCGTGACCGGACA 369
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                                                                               121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                             370 CGAGGCCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 426
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APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Franke, Knut
APPLICANT: Frimpong, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
FRIOR RELING DATE: 2003-07-18
PRIOR PLILNG DATE: 2003-07-18
PRIOR PLILNG DATE: 2002-07-18
PRIOR PLILNG DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/439,617
PRIOR PLILNG DATE: 2002-07-26
PRIOR PLILNG DATE: 2003-07-24
PRIOR FILING DATE: 2003-06-03
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Version 3.2
SEQ ID NO 126
LENGTH: S60
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US-09-896-888A-1
; Sequence 1, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
; FILE REPRENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896,888A
; CURRENT FILING DATE: 2001-66-29
; PRIOR APPLICATION NUMBER: US/09/048,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: OPIE2 promoter sequence US-10-622-088-126
                                                                                                                                                                                                                                                   Sequence 126, Application US/10622088; Publication No. US20040219516A1; GENERAL INFORMATION: APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown
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351 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 410
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Publication No. US20030185845A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REPERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT APPLICATION NUMBER: US/10/295,074
NUMBER OF SEQ ID NOS: 60
SSQTWARE: Patentin version 3.1
SSQTUARE: Patentin version 3.1
LENGTH: 2773
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                                                                                                                                                                                                                                  Length 564;
                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                  100.0%; Score 177; DB 9;
100.0%; Pred. No. 1.5e-54;
vative 0; Mismatches 0;
049,946
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LOCATION: (561)...(566)
OTHER INFORMATION: HindIII site
PEATURE:
NAME/KEY: misc recomb
LOCATION: (573)...(578)
OTHER INFORMATION: Aval site
                                                                                                                                                               ; ORGANISM: Orgyia pseudotsugata
US-09-896-888A-1
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LOCATION: (1156)..(1161)
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NAME/KEY: misc_recomb
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US-10-846-911-60

i Sequence 60, Application US/10846911

j Publication No. US20040258660A1

i GENERAL INFORMATION:

APPLICANT: KILSER, Finn Stausholm

APPLICANT: HEAST, Tomas

APPLICANT: BRAIT, Tomas

i APPLICANT: WOULBORG, Bjorn

APPLICANT: WOULBORG, Bjorn

APPLICANT: WOURINSEN, Sozen

ITILE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

ITILE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

ITILE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

ITILE OF INVENTION NUMBER: PC/10/046, 911

CURRENT APPLICATION NUMBER: PC/10/0764

PRIOR FILING DATE: 2002-11-15

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: PR 2001 01702

PRIOR APPLICATION NUMBER: PR 2001 01702

PRIOR APPLICATION NUMBER: PR 2001 01702

NUMBER OF SEQ ID NOS: 60

SOFTWARE PATENTING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 60

SEQ ID NO 60

LENGTH: 2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGGTAACCGCAGCCGGACGCAACTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 177; DB 16; Length 2773; Best Local Similarity 100.0%; Pred. No. 1.9e-54; Matches 177; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                         NAME/KEY: misc recomb
LOCATION: (212B)..(2133)
OTHER INFORMATION: PatI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: AvaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: AvaI site
LOCATION: (2294)..(2299)
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LOCATION: (561)...(566)
OTHER INFORMATION: HindIII site
PEATURE:
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NAME/KEY: misc recomb
LOCATION: (2551)..(2556)
COTHER INFORMATION: Apall site
US-10-295-074-60
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ORGANISM: Artificial sequence
OTHER INFORMATION: ApaLI site
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355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGAGGCAGCACTCCT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 CGAGGCCCCGTCCCGCTTATCGCGCCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 89, Application US/10622088
Publication No. US20040219516A1
GENERAL INFORMATION:
APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
                                            FEATURE:
NAME/KEY: misc_recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_recomb
LOCATION: (1155)..(1161)
OTHER INFORMATION: Apall site
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NAME/KEY: misc_recomb

LOCATION: (2551)..(2556)

OTHER INFORMATION: Apail site
US-10-846-911-60
                                                                                                                                                                         NAME/KEY: misc_recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
FEATURE:
                                                                                                                                                                                                                                                                           NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
LOCATION: (573)...(578)
OTHER INFORMATION: Aval site
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NAME/KEX: misc recomb
LOCATION: (629)\( \times \). (634)
OTHER INFORMATION: Cla1 site
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Gaps

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APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0920.545007
CURRENT FILING DATE: 2003-07-18
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/396,135
PRIOR APPLICATION NUMBER: US 60/396,17
PRIOR PELING DATE: 2002-07-18
PRIOR PELING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2003-07-19
PRIOR PLICATION NUMBER: US 60/427,231
PRIOR PLICATION NUMBER: US 60/427,231
PRIOR PRILING DATE: 2003-03-03-04-04
PRIOR PILING DATE: 2003-03-03-04
PRIOR PILING DATE: 2003-03-03-04
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Version 3.2
LENGTH: 325
LENGTH: 325
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                                                                                                                                            FEATURE: OTHER INFORMATION: Recombination region of pIB/V5-His-DEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Recombination region of pIB/V5 His DEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 18;
Pred. No. 8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.2%; Score 41; DB Best Local Similarity 100.0%; Pred. No. 8e-Matches 41; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                  NAME/KEY: misc feature
; LOCATION: (141)..(148)
; OTHER INFORMATION: n may be any nucleotide
US-10-622-088-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (141)...(142)
OTHER INFORMATION: n is a, c, g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 149, Application US/10622088 Publication No. US20040219516A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J. APPLICANT: Harwood, Steven
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Madden, Knut
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Best Local Similarity 100.
Matches 41; Conservative
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; LOCATION: (145)..(276)
US-10-622-088-149
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                     LENGTH: 147
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007

CURRENT APPLICATION NUMBER: US/10/622,088

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: PCT/US03/22437

PRIOR APPLICATION NUMBER: PCT/US03/22437

PRIOR APPLICATION NUMBER: US 60/396,335

PRIOR PILING DATE: 2002-07-18

PRIOR PILING DATE: 2002-07-26

PRIOR PILING DATE: 2002-07-26

PRIOR PILING DATE: 2002-11-19

PRIOR PILING DATE: 2003-11-19

PRIOR PILING DATE: 2003-03-24

PRIOR PILING DATE: 2003-03-24

PRIOR PILING DATE: 2003-03-24

PRIOR PILING DATE: 2003-03-24

PRIOR PILING DATE: 2003-03-34

PRIOR PILING DATE: 2003-03-35

PRIOR PILING DATE: 2003-03-36

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harwood, Steven
APPLICANT: Madden, Knut
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
IIILE OF INVENTION: Viral Vectors Containing Recombination Sites
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CURRENT APPLICATION NUMBER: US/10/622,088

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: PCT/US03/22437

PRIOR FILING DATE: 2003-07-18

PRIOR FILING DATE: 2003-07-18

PRIOR FILING DATE: 2002-07-18

PRIOR PLING DATE: 2002-07-26

PRIOR PLING DATE: 2002-07-26

PRIOR PLING DATE: 2002-11-19

PRIOR PLING DATE: 2002-11-19

PRIOR PLING DATE: 2002-11-19

PRIOR PLING DATE: 2002-11-19

PRIOR PLING DATE: 2003-11-19

PRIOR PLING DATE: 2003-11-19

PRIOR PLING DATE: 2003-03-24

PRIOR PLING DATE: 2003-03-24

PRIOR PLING DATE: 2003-03-34

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Publication No. US20040219516A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: pIB/VS-His-DEST
US-10-622-088-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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8 셤 ò 셤 ò Gaps

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Query Match
Best Local Similarity
Matches 48; Conserva
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                                                                                                                                                                                                                                                                                 RESULT 11
US-10-369-493-45503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.2; Di
Pred. No. 0.22,
0; Mismatches
GENERAL INFORMATION:
PUBLICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: INFEDA, HARUO
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIKAWA, HAROSHI
APPLICANT: SHIKAWA, HAROSHI
APPLICANT: SHIKAWA, HAROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQUENCE 1, Application US/10156761
FUBLICATION NO. US20030119018A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
ITILE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.2
Best Local Similarity 61.2
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | PEATURE:
| NAME/KEY: CDS
| LOCATION: (1)..(3138)
| US-10-156-761-2538
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Sequence 42126, Application US/10437963
; Sequence 42126, Application US/10437963
; Publication No. US2040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Shoukharov, Andrey A.
; APPLICANT: Boukharov, Brad
; APPLICANT: Boukharov, Andrey A.
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REPERBRES: 38-2153221B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 42126
; LENGTH: 1116
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45503, Application US/10369493
; Sequence 45503, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INPORMATION:
    APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REPRENCE: 38-10(52052)8
; CURRENT PILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-22
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 45503
LENGTH: 1404
                                                                                                                                                                                    99 ATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCCTATAAATACAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 Accechaececerchaacerececarererecrecececrisecececerrecececaage 523
                                                                                                                          58 CCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGG
   Length 9025608;
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                                                             Indels
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                                                             33;
DB 15;
Score 32.2; DB Pred. No. 0.78; 0; Mismatches
                                                                                                                                                                                                                                                                                        3129547 CCTTGAGGCCTCGTCCAGGTTCTC 3129571
                                                                                                                                                                                                                                                 118 ACACGAGGCGCCCGTCCCGCTTATC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Rhodobacter capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 CCCGCAACGATCTGGTA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524 ACCGCGACGATCTGGAA 540
   Query Match
Best Local Similarity 61.2%;
Matches 52; Conservative
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sequence 30 , John Color (1) cation US/10221613

publication No. US20040029123A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurf
ITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
FILE REPERBROCE: 5013.1004
CURRENT APPLICATION NUMBER: US/10/221,613
PRIOR APPLICATION NUMBER: PCT/EP01/02945
DE 10019058.8
DE 10019058.8
DE 10019058.8
DE 10035259.7
PRIOR PITTER.
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                                APPLICANT: MILEMANT: MILEMANT: MILEMANT: MILEMANT: MICHOLAS
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Aby Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-ND
CURRENT APPLICATION NUMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR PILING DATE: 2002-04-04
PRIOR PILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList,pl version 3.0.4 (C) 2001 Syngenta
LENGTH: 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 TGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCTCCCCTTATCGCGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 657;
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Pred. No. 1.1;
0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-03-15
2000-03-15
2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.43
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72; Conservative
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SEQ ID NO 303
LENGTH: 6107
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APPLICANT: La Rosa, Thomas J.

APPLICANT: Ea Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPEBENCE: 38-21 (53221)

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 55473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1543 AACGTCATCGAGCAGCCGCTCCGCTTCCCCTCCGACGCCCCCAGCGCCCCTCGCGCGT 1602
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                                                                                                                                                                                                               16 GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 AACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                              76 COCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 130
                                                                                                                                                                                                                                                                                                                                                    Score 30.2; DB 18; Length 2472;
Pred. No. 1.1;
0; Mismatches 48; Indels 0;
                                                                                                                   Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1603 GACCTCATCCGCGGCCTGCTCGACGAGCCCCCACAAGCGGATCGC 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 TATCTCATGCGCGTGACCGGACACGAGGCGCCCGGTCCCGCTTATCGC 144
                                                                                                              Score 30.2; DB 18; Length
Pred. No. 1;
0; Mismatches 53; Indels
                                          , OTHER INFORMATION: Clone ID: PAT_MRT4530_45406C.1
US-10-437-963-42126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_57478C.1
US-10-437-963-55473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)..(2472)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 563, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 55473, Application US/10437963
Publication No. US20040123343A1
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Best Local Similarity 55.1%;
Matches 59; Conservative (
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1 Similarity 53.9%;
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
ORGANISM: Oryza sativa
                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                  pna/US103A_COMB.seq:
pna/US103B_COMB.seq:
                                                                                                                                                                                                                                                                                                                                                                pna/US108A_COMB.seq:
/cgn2_6/ptodata/1/pna/US6046
                                                                                                                          May 10, 2005, 04:33:07; Search time 1465.23 Seconds (without alignments) 4931.434 Million cell updates/sec
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10: /cgn2_6/prodata/1/pna/USO8_COMB.seq:*

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19: /cgn2_6/prodata/1/pna/USO9_COMB.seq:*

10: /cgn2_6/prodata/1/pna/USO9_COMB.seq:*

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/cgn2_6/ptodata/1/pna/US099D_COMB.seq
/cgn2_6/ptodata/1/pna/US099E_COMB.seq
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                              45554873 segs, 20411521753 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                       nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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B\_COMB.seq:\* C\_COMB.seq:\* \_COMB.seq:\*

COMB.seq:\*

COMB.seq:\*

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117: /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## UMMARIES

|               |       | de    |        |     | SOMETES              |                   |
|---------------|-------|-------|--------|-----|----------------------|-------------------|
| Result<br>No. | Score | Query | Length | DB  | ΩI                   | Description       |
| -             | 177   | 100.0 | 462    | 191 | US-09-048-911-14     | Sequence 14, Appl |
| 7             | 177   | 00    | 9      | 38  | -09-896-88           | e 14,             |
| m             | 177   | 100.0 | 462    | 38  | 888-968              | 14,               |
| 4             | 177   | 100.0 | 9      | ~   | 303-22437-12         | 126,              |
| ß             | 177   | ö     | 260    |     | 522-088-12           | e<br>1            |
| 9             | 177   | 100.0 |        |     | 9-048-               | e 1,              |
| 7             | 177   | 00    | 9      | 38  | 9-896-88             | e 1,              |
| <b>60</b>     | 177   | 100.0 | 9      |     | 8-9                  | e 1,              |
| 6             | 177   |       | 77     | 21  | 074-6                | e 60,             |
| 10            | 177   | 0     | 77     |     | 46-911-6             | e 60,             |
| 11            | 175.4 | 99.1  | 5038   |     | JS03-22437-          | 89,               |
| . 12          | 75.   | φ.    | 03     | 28  | 2-088-89             | Seguence 89,      |
| 13.           |       | 23.2  | 147    | 7   | -US03-22437-         | 127,              |
| 14            |       | m.    | 147    | 28  | 2-088-12             | equence 127       |
| 15            | 41    | 23.2  | 325    | 28  | 10-622-088-149       | e 149             |
| _             | 34    | σ.    | 2289   | 32  | -09-702-134-1654     | equence 16542,    |
| c 17          | 34    | 19.2  | 2289   | 35  | 09-815-264-          | e 72544           |
| -             | m     | ď.    | 2322   |     | -09-620-392-920      | equence 920, Ap   |
| Н             | ë     | œ.    | 49     |     | 9-293-972-299        | e 29963,          |
| 7             | e     | φ.    | 49     |     | 19-904-939-2996      | equence 29963     |
| 21            | 32.4  | 18.3  | 119    | 46  | 0-015-127-518        | Sequence 5182, Ap |
| c 55          | N     | Θ.    | 2520   |     | 10-015-127-51        | equence 514,      |
| 23            | N     | ω.    | 4861   |     | -620-392-2289        | e 22894           |
| 24            | N     | 8     | 4861   | 32  | 9-702-134-275        | equence 27502     |
| 25            | 'n.   | œ     | 4861   |     | -815-264-8137        | e 8137            |
| c 26          | 2     | 8     | 313    | 49  | )-156-761-253        | 2538              |
| 27            | 7     | ω.    | 90256  | 4   | -10-156-76           | ce 1,             |
| 7             | 32    | 8     | 92     | 20  | 09-313-292-246       | equence 2465      |
| c 29          | 32    | 18.1  | 921    | 62  | US-10-779-543-8561   | 8561              |
| 30            | Η.    | .'    | 418    | 27  | 9-606-977-5909       | 5903              |
| 31            | 31.4  | 17.7  | 418    | 83  | 50-141-233-590       | 5903              |
| 32            | 31.4  | 17.7  | 425    | 36  | 9-837-604A-433       | Sequence 43377, A |
| 33            | 31.4  | 17.7  | 425    | 36  | 09-837-604B-433      | 4337              |
| 34            |       | 17.7  | 425    | 88  | -60-1                | 4026              |
| . 35          | 30.8  | 17.4  | 1268   | 27  | 4                    | e 2544            |
| 36            | 0     | 17.4  | 1268   | 27  | US-09-614-150A-25442 | e 2544            |
| 37            | 0     | 17.4  | 1268   | 98  | US-60-173-464-21087  | e 2108            |
| 38            |       | 17.4  | 26     | 88  | -60-191-637-         | e 2556            |
| 39            | 0     | 17.4  | 1268   | 88  | 1-2017               | e 2017            |
| 40            | 0     | 17.4  | 34     | 27  | -09-614-150-3849     | equence 3849      |
| 41            | ö     | 17.4  | 34     |     | -09-614-150A-38      | e 3849            |
| 42            |       | 17.4  | 4      | 88  | -60-191-637-3812     | equence 3812      |
| 4             | 。     | 17.4  | 44     |     | S-09-614-150-3849    | equence 3849      |
| c 44          | 30.8  | 17.4  |        | 27  | -09-614-150A-3       | Sequence 38494, A |
| 4             | 30.8  | 17.4  | 3448   |     | 60-191-637-3812      | equence 381       |

250 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 309 61 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 120 61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 120 310 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 369 09 9 CGAGGCGCCCGTCCCGCTTATCGCCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177 370 cgaggcgcccgrcccgcrrarcgcgccraraarracagcccgcaacgarcrggraaa 426 1 GTCTTATCGTGACGCGCGCGCGTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 1 GICITAICGIGACAGGACGCCAGCTICCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT Gaps ; 0 ö FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Promoter OTHER INFORMATION: sequence of the OpMNPV ie2 gene of Artificial Sequence:Promoter the OpMNPV ie2 gene 100.0%; Score 177; DB 38; Length 462; 100.0%; Pred. No. 1.3e-44; Length 462; Indels Score 177; DB 16; Pred. No. 1.3e-44; APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44 CURRENT APPLICATION NUMBER: US/09/048,911 CURRENT FILING DATE: 1998-03-26 EARLIER PRILIGE DATE: 1997-03-27 NUMBER OF SEQ ID NOS: 50 SOFTWARE PARENTIN VECTOR SEQ ID NOS: 50 SEQ ID NO 14 LENGTH: 462 APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44 FURRENT APPLICATION NUMBER: US/09/896,888 CURRENT APPLICATION NUMBER: US/09/896,888 CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US 60/048,911 PRIOR APPLICATION NUMBER: US 60/049,946 PRIOR APPLICATION NUMBER: US 60/049,946 PRIOR FILING DATE: 1997-03-27 NUMBER OF SEQ ID NOS: 50 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 14 LENGTH: 462 Mismatches 0; Mismatches ; Sequence 14, Application US/09896888; GENERAL INFORMATION: Sequence 14, Application US/09048911 GENERAL INFORMATION: , , OTHER INFORMATION: Description; OTHER INFORMATION: sequence of US-09-896-888-14 100.0%; Query Match Best Local Similarity 100.0%; Matches 177; Conservative TYPE: DNA ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence Query Match 100. Best Local Similarity 100. Matches 177; Conservative US-09-048-911-14 US-09-896-888-14 121 TYPE: DNA FEATURE: Db ð В 8 ò ò ŝ

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TYPE: DNA
ORGANISM: Unknown
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FEATURE:
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310 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 369
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                                                                        370 CGAGGCGCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 426
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: INVIETORGEN Corporation
TITLE OF INVIETOR CORPORATION:
FILE REFERENCE: 0942.545PC07
CURRENT APPLICATION NUMBER: PCT/US03/22437
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PILING DATE: 2002-07-18
PRIOR PELING DATE: 2002-07-26
PRIOR PELING DATE: 2002-07-26
PRIOR PELING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2003-13-34
PRIOR PLING DATE: 2003-13-34
PRIOR PLING DATE: 2003-06-03
PRIOR PLING DATE: 2003-06-03
PRIOR PLING DATE: 2003-06-03
                                               121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA
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CTHER INFORMATION: Description of Artificial Sequence:Promoter:
CTHER INFORMATION: sequence of the OpMNPV ie2 gene
US-09-896-888A-14
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                                                                                                                                                                                                                                                        APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REPERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 462
                                                                                                                                                                                                           Sequence 14, Application US/09896888A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn version 3.2
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ORGANISM: Unknown
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                                                                                                                                                                 RESULT 3
US-09-896-888A-14
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LENGTH: 560
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APPLICANT: Franke, Kenneth
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT FILING DATE: 2003-07-18
PRIOR PAPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR PLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2003-07-36
PRIOR FILING DATE: 2003-07-36
PRIOR FILING DATE: 2003-07-36
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PRIOR PLING DATE: 2003-07-36
PRIOR PLING DATE: 2003-06-03
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                                                                                                             Length 560;
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100.0%; Pred. No. 1.3e-44;
tive 0; Mismatches 0;
                                                                                                         Query Match
100.0%; Score 177; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 177; Conservative 0; Mismatches 0;
, OTHER INFORMATION: OpIE2 promoter sequence PCT-US03-22437-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 126, Application US/10622088 GENERAL INFORMATION:
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SEQ ID NO 126
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Matches 177; Conservative
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US-09-896-888A-1
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100.0%; Score 177; DB 38; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 177; Conservative 0; Mismatches 0; Indels 0
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Sequence 1, Application US/09896888
GENERAL INFORMATION:
JULICANT: The University of British Columbia APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/896,888
PRIOR APPLICATION NUMBER: US 60/048,911
PRIOR APPLICATION NUMBER: US 60/049,946
PRIOR APPLICATION NUMBER: US 60/049,946
PRIOR FILING DATE: 1999-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 564
                                                                           APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/048,911
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: US 60/049,946
EARLIER APPLICATION NUMBER: US 60/049,946
SARLIER APPLICATION NUMBER: US 60/049,946
SARLIER APPLICATION NUMBER: US 60/049,946
SARLIER APPLICATION NUMBER: DS 60/049,946
SOFTWARE: Patentin Ver. 2.0
                  Sequence 1, Application US/09048911
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA; ORGANISM: Orgyia pseudotsugata
US-09-048-911-1
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; ORGANISM: Orgyia pseudotsugata
US-09-896-888-1
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
US-09-048-911-1
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TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILLE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT PILLING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
LENGTH: 2773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 177; DB 38;
100.0%; Pred. No. 1.3e-44;
tive 0; Mismatches 0;
Sequence 1, Application US/09896888A

Sequence 1, Application US/0989688A

Sequence 1, Application Sequence 1, Application Sequence 1, The University of British Columbia TITLE OF INVENTION Insect Expression Vectors FILE REFERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/046,911

FRIOR FILING DATE: 1998-03-26

FRIOR FILING DATE: 1998-03-26

FRIOR FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 1

LIENGTH: 564
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Orgyia pseudotsugata
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NAME/KRY: misc_recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.
Matches 177; Conservative
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61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACA 120
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                                                                          OTHER INFORMATION: p2ZOp2F expression vector for insect cells
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OTHER INFORMATION: HindIII site
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LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal,
TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KRY: misc_recomb
LOCATION: (593). (598)
OTHER INFORMATION: BamHI site
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LOCATION: (2551)..(2556)
OTHER INFORMATION: ApaLI site
US-10-846-911-60
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NAME/KEY: misc_recomb
LOCATION: (1155)..(1161)
OTHER INFORMATION: Apall site
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NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: P&tI site
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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NAME/KEY: misc_recomb
LOCATION: (625)..(630)
OTHER INFORMATION: Clal site
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LOCATION: (629)...(634)
OTHER INFORMATION: ClaI site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
FEATURE:
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OTHER INFORMATION: ECORI
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LOCATION: (586)..(591
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LOCATION: (561)..(566
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APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: BRATT, Tomas
APPLICANT: WOLLBORG, Bjorn
APPLICANT: WOURTSEN, Soren
TITLE OF INVENTION: NOVEL IMMUNGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: 674542-2018
CURRENT APPLICATION NUMBER: US/10/846,911
CURRENT PILING DATE: 2004-05-14
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
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SOFTWARE: PARCHING DATE: 2001-11-16
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NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
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US-10-846-911-60
; Sequence 60, Application US/10846911
; GENERAL INFORMATION:
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LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
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LOCATION: (2551)..(2556)

OTHER INFORMATION: ApaLI site

US-10-295-074-60
                                                                  FEATURE:
NAME/KEY: misc_recomb
LOCATION: (629)..(634)
OTHER INFORMATION: Clai site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
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NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
WAME/KEY: misc recomb
LOCATION: (625)..(630)
WHER INFORMATION: Clal site
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GCCATION: (2204)...(2209)
THER INFORMATION: NGOI site
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                  LENGTH: 5038
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 SEQ ID NO 89
                                                                                                                                            Query Match
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PRIOR PPLICATION NUMBER: US/10/622,088

PRIOR PLILNG DATE: 2003-07-18

PRIOR PLILNG DATE: 2003-07-18

PRIOR PLILNG DATE: 2002-07-18

PRIOR PLILNG DATE: 2002-07-18

PRIOR PLILNG DATE: 2002-07-26

PRIOR PLILNG DATE: 2002-11-19

PRIOR PLILNG DATE: 2002-11-19

PRIOR PLILNG DATE: 2003-11-19

PRIOR PLILNG DATE: 2003-03-24

PRIOR PLILNG DATE: 2003-03-24

PRIOR PLILNG DATE: 2003-03-04-05

PRIOR PLILNG DATE: 2003-03-04-05

PRIOR PLILNG DATE: 2003-05-03-04-05

PRIOR PLILNG DATE: 2003-06-03
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sequence 89, Application PC/TUS0322437
GENERAL INFORMATION:
APPLICATION
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                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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APPLICANT: Madden, Knut
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LENGTH: 5038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                 951 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFREENCE: 0942.545F00.

CURRENT APPLICATION NUMBER: PCT/US03/22437

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: US 60/396,335

PRIOR FILING DATE: 2002-07-26

PRIOR FILING DATE: 2002-07-18

PRIOR PLICATION NUMBER: US 60/398,617

PRIOR PRILING DATE: 2002-11-19

PRIOR PLILING DATE: 2002-11-19

PRIOR PRILING DATE: 2003-03-24

PRIOR PRILING DATE: 2003-03-24

PRIOR FILING DATE: 2003-04-03

NUMBER OF SEQ ID NOS: 146

SEQ ID NO 127
                                                                                                                                                                             Score 175.4; DB 58; Length 5038;
Pred. No. 5.5e-44;
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                                                                                                                                                                                                                                             1; Indels
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100.0%; Pred. No. 0.036;
tive 0; Mismatches 0
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| LOCATION: (141)...(148)
| OTHER INFORMATION: n may be any nucleotide
| PCT-US03-22437-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 127, Application PC/TUS0322437 GENERAL INFORMATION:
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                                                                                      ) OTHER INFORMATION: pIB/V5-His-DEST
US-10-622-088-89
                                                                                                                                                                                99.1%;
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                             Best Local Similarity 99.4
Matches 176; Conservative
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (141)..(142)
OTHER INFORMATION: n is a, c, g, or
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                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (145)..(276)
US-10-622-088-149
                        ORGANISM: Artificial
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APPLICANT: Brimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-04-05
PRIOR PILING DATE: 2003-06-03
                                    APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.545000/00/05/0088
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Recombination region of pIB/V5-His-DEST
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PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR PILING DATE: 2003-07-18
PRIOR PLILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2002-07-8
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-32
PRIOR PILING DATE: 2003-06-03
PRIOR FILING DATE: 2003-06-03
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PRIOR FILING DATE: 2003-06-03
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SEQ ID NO 149
LENGTH: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J. APPLICANT: Harwood, Steven APPLICANT: Madden, Knut
Harwood, Steven
Madden, Knut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-622-088-149
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FEATURE: OTHER INFORMATION: Recombination region of pIB/V5 His DEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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Sequence 25442, A
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Sequence 25441, A
Sequence 35, Appl
Sequence 15, Appl
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Sequence 26108, A
Sequence 26107, A
Sequence 1101, Ap
Sequence 52210, A
Sequence 6584, Ap
Sequence 518, App
Sequence 518, App
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Sequence 401, App
Sequence 499, App
                                                                                                   May 10, 2005, 05:51:35 ; Search time 436.346 Seconds (without alignments) 834.449 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
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4: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*
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6: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-11-097-143-25422
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PCT-USO5-07924-35
PCT-USO5-07924-1
US-11-075-185-35
PCT-USO5-07924-1
US-10-517-441-401
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US-10-717-143-26108
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| Sequence 1239, Ap Sequence 11844, A Sequence 14117, Ap Sequence 7217, App Sequence 674, App Sequence 28994, A Sequence 21313, A Sequence 621, App Sequence 1146, A Sequence 1430, App Sequence 5, Appli Sequence 1, Appli Sequence 647, Appli Sequence 647, Appli Sequence 647, Appli Sequence 641, Appli Appli Sequence 641, Appli Appli Sequence 641, Appli | sedneuce 3/3                      | gainst TNP-alpha   |
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| US-11-031-175-1239<br>US-60-659-397-11844<br>US-10-450-763-14117<br>US-11-031-175-7217<br>US-11-031-175-674<br>US-10-703-032-28934<br>US-10-703-032-28935<br>US-11-031-175-621<br>US-11-031-175-621<br>US-11-031-175-621<br>US-11-097-143-27146<br>US-11-097-143-27145<br>PCT-USO-132-136<br>US-11-109-143-1<br>US-11-109-143-1<br>US-11-109-143-1<br>US-11-03-13-145<br>US-11-109-143-1<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-13-145<br>US-11-03-145-145  | US-1U-9/2-0/9-3/529<br>ALIGNMENTS | dolf  Henriette  Birk  D310/939,107  99-10  17/DK03/00147  11  11  11  12  13  14  15  16  16  17  16  17  17  18  19  10  10  10  10  10  10  10  10  10  |
| 16.2 25048 11<br>16.2 215013 13<br>15.9 2892 11<br>15.9 2892 11<br>15.7 570 9<br>15.7 570 9<br>15.7 2208 11<br>15.7 5288 11<br>15.5 601 9<br>15.5 1707 8<br>15.5 543 1<br>15.5 543 1<br>15.5 543 1<br>15.5 67323 1  | 000                               | n US/1  rate Rusher Rusher Rusher Rusher Rusher Rusher Rusher For Submitted Rusher Rus |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   |                                   | RESULT 1  Sequence 60, Applicatio GENERAL INFORMATION: APPLICANT: Pedersen, APPLICANT: Beefr, Bla APPLICANT: Beefren, TITLE OF INVERTION: NO FILE REFERENCE: 674542 CURRENT APPLICATION NUMB PRIOR FILING DATE: 200 PRIOR PILING DATE: 200 CURRENT: 2773 TYPE: DN OTHER INFORMATION: DS: FEATURE: NAME/KEY: misc_recomb LOCATION: (543)(559) OTHER INFORMATION: AV FEATURE: NAME/KEY: misc_recomb LOCATION: (586)(591) OTHER INFORMATION: AV FEATURE: NAME/KEY: misc_recomb LOCATION: (586)(591) OTHER INFORMATION: AV FEATURE: NAME/KEY: misc_recomb LOCATION: (586)(591) OTHER INFORMATION: AV FEATURE: NAME/KEY: misc_recomb LOCATION: (588)(598) OTHER INFORMATION: Ba COTHER INFORMATION: Ba   |

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657 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 716
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        717 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 762
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55.7%; Pred. No. 4.8;
tive 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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Pred. No. 4.8;
0; Mismatches
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25442
LENGTH: 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DAPE: 2000-03-23
NUMBER OF SEQ ID NOS: 4300B
SOFTWARE: PASISEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/157,832

PRIOR PILING DATE: 1999-10-05

PRIOR PELLOR DATE: 1999-10-19

PRIOR PELLOR DATE: 1999-10-19

PRIOR PELLOR DATE: 1999-10-19

PRIOR PELLOR DATE: 1999-10-28

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PELLOR DATE: 1999-11-12

PRIOR PELLOR DATE: 1999-11-12

PRIOR PELLOR DATE: 1999-11-28

PRIOR PELLOR DATE: 2000-01-12

PRIOR PELLOR DATE: 2000-01-12

PRIOR PELLOR DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38495, Application US/11097143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      17.4%;
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                             ; ORGANISM: DROSOPHILA
US-11-097-143-25442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: DROSO
US-11-097-143-38495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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PAPPLICANI: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DRESPECTION EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR PLICATION NUMBER: 60/164,769

PRIOR FILING DATE: 1999-11-12

PRIOR PRIOR PLICATION NUMBER: 60/175,693

PRIOR FILING DATE: 1000-01/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 TATCGGAACAGGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 177; DB 7;
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 177; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25442, Application US/11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/184,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (255<u>T</u>)..(2556)
; OTHER INFORMATION: Apal site
US-10-939-107-60
                                                                                                                                                                                                                                                                             LOCATION: (1156)..(1161)
OTHER INFORMATION: ApalI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: Pstl site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME TO THE TRANSPORT OF THE TRANSPORT O
                                                                                                                LOCATION: (629)..(634)
OTHER INFORMATION: Clal site
OTHER INFORMATION: ClaI site
                                                                    NAME/KEY: misc recomb
LOCATION: (629)..(634
                                                                                                                                                                                                                                 NAME/KEY: misc recomb
LOCATION: (1156)..(11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc recomb
LOCATION: (2294)..(22
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TYPE: DNA ORGANISM: DROSOPHILA
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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/161,338
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,693
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
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                                                 APPLICANT: Vencer, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: BETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
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0; Mismatches
                                                                                                                                                                                TITLE REFERENCE: CLOOO726
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PILIC BATE: 2005-04-04
PRIOR PRICATION NUMBER: US/11/097,143
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-12
PRIOR PRILING DATE: 1999-11-12
PRIOR PRILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PRILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-2
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
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Pred. No. 5.
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SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 38494, Application US/11097143 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Conservative
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Matches 59; Conserv
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US-11-097-143-25441/c
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LENGTH: 3448
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Sequence 35, Application PC/TUSO507924
GENERAL INFORMATION:
APPLICANT: REEVES, CHRISTOPHER D
APPLICANT: REID, BRYAN
APPLICANT: RID, RALPH
TITLE OF INVENTION: BLOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
FILE REFERENCE: 010099.03
FURRENT FILING DATE: 2005-03-17
PRIOR PLICATION NUMBER: US 60/551,103
PRIOR PLICATION NUMBER: US 60/551,103
PRIOR PLICATION NUMBER: US 60/560,290
PRIOR PLILNG DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
SETUMBER: 035-03-06
SEQ ID NO 35-06
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APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GCCTCCATATCAGCGGGGTTATCTCATGCGGGTGACCGGACACG 122
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Pred. No. 5.2;
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Pred. No. 6.6;
0; Mismatches
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PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR PPLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 25441
LENGTH: 3600
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TYPE: DNA
CREANISM: Sorangium cellulosum
PCT-US05-07924-35
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17.3%;
Best Local Similarity 53.3%;
Matches 88; Conservative
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Best Local Similarity 55.7%;
Matches 59; Conservative
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SEQ ID NO 1
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| GENERAL INFORMATION: | APPLICANT: REEVES, CHRISTOPHER D | APPLICANT: REEVES, CHRISTOPHER D | APPLICANT: REEVES, CHRISTOPHER D | APPLICANT: JULIEN, BRYAN | APPLICANT: TILE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS | FILE REFERENCE: 010099.03 | FURRENT APPLICATION NUMBER: PCT/US05/07924 | CURRENT FILING DATE: 2005-03-17 | PRIOR PELICATION NUMBER: US 60/551,103 | PRIOR PELICATION NUMBER: US 60/568,290 | PRIOR FILING DATE: 2004-03-08 | PRIOR PRIOR PRIOR DATE: 2004-03-08 | PRIOR PRIOR DATE: 2004-03-08 | PRIOR PRIOR PRIOR DATE: 2004-03-08 | PRIOR PRIOR DATE: 2004-03-04 | PRIOR PRIOR DATE: 2004-03-04 | PRIOR DAT
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Pred. No. 6.6;
0; Mismatches 74; Indels 3;
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FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Version 3.3
LENGTH: 10968
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Sorangium cellulosum
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; ORGANISM: Sorangium cellulosum
PCT-USOS-07924-1
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1 Similarity 53.3%;
88; Conservative
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Matches 88; Conserv
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RESULT 9

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### AFPLICANT: HORELER, Heinz
| TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
| TITLE OF INVENTION: POOLIFERALIVE disorders |
| TITLE OF INVENTION: POOLIFERALIVE disorders |
| FILE REFERENCE: 47675-93 |
| CURRENT APPLICATION NUMBER: US/10/517,441 |
| CURRENT APPLICATION NUMBER: US/10/517,441 |
| PRIOR FILING DATE: 2004-12-11 |
| PRIOR FILING DATE: 2003-10-01 |
| PRIOR FILING DATE: 2003-00-01 |
| PRIOR FILING DATE: 2003-01-07 |
| TRIESTATE OF SEQ ID NOS: 2147 |
| TYPE: DNA
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                                                                             APPLICANT: ULLEN, BRYAN
APPLICANT: REID, RALPH
TILLEO FO INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
FILE REPERENCE: 010099-03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT APPLICATION NUMBER: US 60/551,103
PRIOR PILING DATE: 2004-03-08
PRIOR PELING DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 78869;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
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Pred. No. 7.7;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
Sequence 1, Application US/11075185
GENERAL INFORMATION:
APPLICANT: REEVES, CHRISTOPHER D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1
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Best Local Similarity 53.3%;
Matches 88; Conservative
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MODEL, Fabian
NIMMRICH, Inko
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MARX, Almuth
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goldman, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
CURRENT APPLICATION NUMBER: US/11/031,175
CURRENT APPLICATION NUMBER: G0/217,883
FRIOR APPLICATION NUMBER: G0/217,883
FRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2371
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR PAPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-28

PRIOR PLING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR PLING DATE: 2000-02-23

NUMBER OF SEQ ID NOS: 43008

SEQ ID NO 26108

SEQ ID NO 26108

LENGTH: 1799

TYPE: DNA

ORGANISM: DROSOPHILA
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Pred. No. 9.7;
0; Mismatches 47; Indels 0;
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                          1465 CACTTCCTCCCAAPATCGCGCC 1444
      126 CGCCCGTCCCGCTTATCGCGCC 147
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Best Local Similarity 55.2%;
Matches 58; Conservative
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CRGANISM: Myxococcus xanthus
US-11-031-175-2371
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TITLE OF INVENTION: proliferative disorders

FILE REFERENCE: 47675-93

CURRENT APPLICATION NUMBER: US/10/517,441

CURRENT FILING DATE: 2004-12-11

PRIOR FILING DATE: 2003-010-01

PRIOR PILING DATE: 2003-01-07

PRIOR PILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01

PRIOR FILING DATE: 2003-10-01
                                                                                                                                                                                                                                                                                                               2079 AACGCGAAACCACCGCTCCTCGCTCTCCAACCGCCGGAATAACTCAACCGCC 2020
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                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-517-441-401
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                                                                                                                                             Query Match 16.9%; Score 30; DB 8; Length 3107; Best Local Similarity 50.7%; Pred. No. 9; Matches 72; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 8; Length 3501;
Pred. No. 9.1;
0; Mismatches 70; Indels
                                                                                                                                                                                                       70; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 50.7%;
Matches 72; Conservative
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SCHMITT, Manfred
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MARX, Almuth
HOEFLER, Heinz
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HARBECK, Nadia
KOENIG, Thomas
MAIER, Sabine
MARTENS, John
MODEL, Fabian
NIWMRICH, Inko
RUJAN, Tamas
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US-10-517-441-499/c
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US-11-031-175-1101/c
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ADOSOPHILA GENES.
FILE REFERENCE: CL000728
                                                                                                          Gaps
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                                                      16.8%; Score 29.8; DB 10; Length 1789; larity 49.1%; Pred. No. 9.9; Conservative 0; Mismatches 82; Indels 0;
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Best Local Similarity 49.1%; Pred. No. 11;
Matches 79; Conservative 0; Mismatches 82;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/097,143 CURRENT FILING DATE: 2005-04-04
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PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR PEDICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-11-12
PRIOR PLICATION NUMBER: 60/173,383
PRIOR PELICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-28
PRIOR PELICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-097-143-26107/c
; Sequence 26107, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/184,831
FILING DATE: 2000-02-24
APPLICATION NUMBER: 60/191,637
FILING DATE: 2000-03-23
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US-11-097-143-26107
                                                                           Best Local Similarity
Matches 79; Conserv
US-11-097-143-26108
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RESULT 15

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Mdfrt3037 UI-CF-DU1

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Minimum DB Maximum DB

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Result Š Searched:

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Title: Perfect

Run on:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and
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sapiens genomic clone Plate=2266 Col=15 Row=A, genomic survey
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 5.1;
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
|mol_type="gamomic DNA"
| Mol_type="gamomic DNA"
| Mol_tref="taxon:5606"
| Al_one="Plate=2266 Col=15 Row=A"
                                                                                                                                                                                                                                                                                                                                           DNA
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 507.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               507 bp
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Plate: 2266 row: A colu
Class: BAC ends
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VERSION
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SOURCE
ORGANISM
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                                                                                   May 10, 2005, 03:45:00 ; Search time 1240.12 Seconds
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          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                     34239544 seqs, 19032134700 residues
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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gb_est2:*
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                              65 GGAACAGGACGCGCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACGAG 124
                                                                      5 TATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATC 64
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                                                                                                                                                                                                                                                              Smail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
       Gaps
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       62; Indels
       Mismatches
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse cull-length cDNA computer-based methods for the mouse cull-length cDNA computer-based sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 06-DEC-2002
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Pleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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                                       Compared with
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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/db_xref="taxon:10090"
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Best Local Similarity 51.7%; Pre
Matches 75; Conservative 0;
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Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Mundtais, L., Okido, T., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numatas, K., Okido, T., Paran, W.J., Pertea, G., Pesole, G., Pesole, G., Perrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sepple, C.A., Setol, M., Shimada, K., Sultana, R., Takraka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Magner, L., Wahlested, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wanghaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazune, N., Harak, T., Rawai, J., Azawa, K., Sakasune, N., Kagwa, I., Miyazaki, T., Wati, K., Sasaki, D., Shibata, R., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
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Email: genome-res@gc.riken.jp, URL:http://genome.gsc.riken.jp/
Hirozand.k., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozand.k., Indiani,Y., India,Y., Kouno,H., Kouno,H.,
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2011)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-184-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokobama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult male liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Division of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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/clone="K630011C08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 402
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PUBMED
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62

3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA

19.0%; Score 33.6; DB 5; Length 402; 51.7%; Pred. No. 5.9; 1.1% 0; Mismatches 70; Indels

Best Local Similarity 51.7 Matches 75; Conservative

Query Match

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CV068875 931 bp mRNA linear EST 24-AUG-2004 f2 new_chopped.fasta.Contig488 Preamplified custom cDNA library in pCMVsport6.1 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY338426 BIKEN full-length enriched, whole joints Mus musculus CDNA clone L230014G21 5', mRNA sequence.
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Eukaryota, Haptophyceae; Isochrysidales; Emiliania.
I (bases 1 to 91).
Wahlund,T.W., Zhang,X. and Read,B.A.
Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying
89 CTTAATGTGATCCCCCCCCCCTTTCCTTTCTCCGTAGCCTGACGCGGCAGCAGCGCCGCTTT 148
                                                                                                       63 TCGGAACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                    149 CCTCACCAGCTCGCACTCTCCTCGGGGCGCACGGCTCGCCGTGCCCCTGCCCACCANGG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 Accrecrecedecedecedesercrecedadadesecedadecededadadesecedadadese
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 348)
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/clone_lib="Preamplified custom cDNA library in
pCNNsport6:1 (ResGen, Invitrogen Inc.)"
/note="Emiliania huxleyi grown in Artificial Seawater
(Guillard's F/2 media)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 ACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTT
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Department of Biological Sciences
California State University San Marcos
133 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA
Tel: 760 750 4129
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Micropaleontology (2004) In press
                                                                                                                                                                                                                                                                                                                                  123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                               209 GACAGAGGGTCCCGCTTCCCTCTCC 233
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Location/Qualifiers
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Mus musculus
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/strain="1516"
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Nikaido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, M., Schonbach, C., Gojobori, T., Baldarelli, R., Hall, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K.W., Blake, J.A., Brade, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibodi, M., Gissi, C., Godzik, A., Gough, J., Garimond, S., Mirochkin, I.V., Lee, Y., Lehnard, B., Lyons, P.B., Maglott, D.B., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lechard, B., Lyons, P.B., Maglott, D.B., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, M., Pontius, J.U., Qi, D., Ramachadran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Hayatsu, N., Hirozane-Kishikawa, Pakakawa, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Wanki, K., Kawai, D., Shibata, K., Shiraki, Y., Sakai, W., Saeaki, D., Shibata, K., Shiraki, A., Sakai, W., Saeaki, D., Shibata, K., Shiraki, A., Sakai, W., Saeaki, D., Shibata, K., Shiraki, A., Sakai, K., Saeaki, D., Shibata, K., Shiraki, A., Sakai, K., Saeaki, D., Shibata, K., Shiraki, A., Sakai, K., Saeaki, D., Saeaki, D., Saeaki, D., Nalaysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNa
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Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKKN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2001)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome_res@ggc.riken.jp, URL:http://genome.gsc.riken.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
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further details.
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Mammalia butnerla; Kodentia; Scillrognath; Muridae; Murinae; Murinae; Mammalia; Euteria; Kodentia; Scillrognath; Murinae; Murinae; Mikaido, 1., Osato, M., Saito, R., Suzuki, H., Yamanakai, I., Kayosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Riyosawa, H., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K., W., Blake, J.A., Bradt, D., Brusic, V., Ratesin, K., Beisel, K., W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gartincich, S., Hirokawa, N., Taraer, K.S., Gaasterland, T., Garaiboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Karaibi, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Karaibi, H., Kawasawa, Y., Lee, Y., Lee, Y., Lee, Y., Lee, Y., Bestole, G., Pertovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ranchandran, S., Ravasi, T., Marchionni, L., Marchach, J.U., Mill, B.L., Konasald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Tarkenaka, Y., Taylor, M.S., Taesdala, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Watanabe, Y., Wang, Y., Watau, J., Aizawa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, Y., Rogers, J., Birner, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Kanalon annotation of 60,770 full-length consoleration for saked on functional annotation of 60,770 full-length consoleration for saked on functional annotation of 60,770 full-length consoleration for saked and 
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
/clone="L230014G21"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brustc, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B. Dragani, T.A., Fletcher, C.F., Forrest, A., Fazer, K.S., Gaasterland, T., Gariboldi, M. (Gissi, C., Godzk, A., Gough, J., Grimmond, S., Gastincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanagi, A., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mixi, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Ring, B.Z., Kingwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Vanger, L., Wallestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yang, L., Yang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Ahizawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Yasai, K., Sasaki, D., Shibata, K., Shiragwa, A., Yasuishi, A., Yasuishizati, Y., Rogers, J., Birney, B. and Haysshizaki, Y., Rasaki, D., Shibata, K., Nakawa, A., Yasuishi, A., Y
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozande,T., Imotani,K., Ishli,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramateu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
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genes. Genome Res. 10 (10), 1617-1630 (2000)
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/cell_line="RCB-0558 LLC"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Fax: 81-45-503-9216
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genoup in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Labbratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues mouse tissues mouse tissues mouse tissues center and Genome Science Labbratory in Riken Prepare mouse tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Prepare
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,K., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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                                                                            genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
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/db xref="taxon:10090"
/clone="L230006D15"
/tissue type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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Pred. No. 9.2;
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Alzawa,K., Akimura,T., Arakawa,T., Carainci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itch,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
                                                                                                                                     3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
                                                                              0; Gaps
             DB 5; Length 354;
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                                     Pred. No. 9.2;
0; Mismatches
          Score 33;
Pred. No.
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Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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BY34318 RIKEN full-length enriched, whole joints Mus musculus cDNA
Glone L230047A12 5', mRNA sequence.
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissues were provided by Vassilis Aidinis (Blomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shizaki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-Length Mouse cDNAs Compared with
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/clone_lib="RIKEN full-length enriched, whole joints"
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Pred. No. 9.2;
0; Mismatches 70
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Matches 75; Conservative 0
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Kawaji, H., Kawasawa, Y., Jackson, I.J., Jarvis, B.D., Kanai, A.,
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Itoh, M., Kagawa, I., Miyazaki, A., Sasaki, M., Sasaki, D., Shibata, K.,
Rogers, J., Birney, E. and Hayashizaki, Y.,
Rogers, J., Birney, E. and Hayashizaki, Y.,
Rogers, J., Birney, E. and Hayashizaki, Y.,
Rogers, J., Dill-Inopth, Danga
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Aizawa.K., Akimura.T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozana,T., Imotani,K., Ishli,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
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Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of captrapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
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Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA computer-based mes sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Pleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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/db xref="taxon:10090"
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MEDLINE PUBMED COMMENT JOURNAL

TITLE

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Gaps ö

Query Match 18.6%; Score 33; DB 5; Length 360; Best Local Similarity 51.7%; Pred. No. 9.2; Matches 75; Conservative 0; Mismatches 70; Indels

FEATURES

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Numeratia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscatura Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dasses 1 to 362)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY339252 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L230021B07 5', mRNA sequence.
BY339252
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99 CTTÅATGTGATCCCCCCCCCTTTCCTTTCTCCGTÄGCCTGACGCGGCAGCAGCGCTTT 158
                                                                                              63 TCGGAACAGGACGCGCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                             Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Ajzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                 123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                     219 GACAGAGCGTCCCCTCTCC 243
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Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pessole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Oi,D., Ramachandran,S.,
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Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
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Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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51.7%; Pred. No. 9.2;
tive 0; Mismatches
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/strain="C57BL/6J"
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2011) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
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Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 371)
S Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikado, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yadi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Golobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Brade, J., Brade, D., Bragin, T. A.,
Fletcher, C., Corbani, L. B., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, Y., Kedzierski, R.,, King, B. L., Konagaya, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.,, King, B. L., Konagaya, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="L230021B07"
/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CITATCGIGACAGGACGCCAGCITCCIGIGITGCIAACCGCAGCCGGACGCAACTCCTIA
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/db_xref="taxon:10090"
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/clone lib="Talr1"
/note="Vector: Lambda ZaplI; mass excised in plasmid
/note="Vector: Lambda ZaplI; mass excised in plasmid
vector pBK-CMV (Stratagene). Site 1: ECORI; Site 2: XhoI;
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf tust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avrl."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ620008 621 bp mRNA linear EST 28-JUN-2002
TaLr1138G03F TaLr1 Triticum aestivum cDNA clone TaLr1138G03F, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sukaryotta, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poodeae; Triticaea; Trong, G. and Walsh, A. Wheat functional genomics - Thatcher Lrl cDNA library Unpublished (2001).
Contact: Dr. Sylvie Cloutier Centact: Dr. Sylvie Cloutier Agriculture and Agri-food Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: (204) 983-2340

Fax: (204) 983-4604

Bmail: scloutier@ac.ca

primer where from the 5' end (same with forward primer and 3'end).

Average insert size is >2.2kb

Plate: 138 row: G column: 03

Seq primer: M13 Forward.
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/mol type="mRNA"
/cultivar="Thatcher Lr1"
constructed by Yulan Piao."
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/tissue_type="Leaf tissue"
/dev_stage="14 Days old"
/lab_host="E. coli XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genefics. National Institute on Aging (NIA), Intramural Research Program, NIH (http://losun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo (dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                 CF916169 1inear EST 05-NOV-2003 B0991A12-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0991A12 IMAGE:30480971 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 611)
Piac, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
Submicrogram amounts of total RNAs by a universal FCR amplification
                        TCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                               171 CCTCACCAGCTCGCACTCTCCTCGGGGGGCACGGCTCGCCGTGCCCTGCCCAGGCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0991 row: A column: 12
Seg primer: M13 Reverse
High quality sequence stop: 611
POLYA=No.
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                                                                                                                                          123 AGGCGCCCGTCCCGCTTATCGCGCC 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dawood B. Dudekula
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/clone lib="Sugano mouse kidney mkia"
/clone lorgan: kidney, Vector: pME186-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [GTTGGCCACTGG], digested
and cloned into distinct DraIII sites of the pWE188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW319335 635 bp mRNA linear EST 25-JAN-2000 unl1f04.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2395039 5' similar to TR:Q9YGPS Q9YGPS RRM-TYPE RNA-BINDING
                                                                                                                                                                                                                                                                                                              152
                                                                                                                                                                                                                                                               63 TCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 635)
Marra,M., Hillier,L., Rucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Sreptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                         62
                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                  3 CTTATCGTGACAGGACGCCAGCTTCCTGTGGTAACCGCAGCCGGACGCAACTCCTTA
                                                                                                                                                                                                                                                                                                            93 cercaccaderedeacerecereceadadeseacecaceaege
                                                                                                                                                                                                                 33 citraarcicarcececececertrecitriceraceraceracecececececece
                                                                                                                        Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                           .;
0
                                                                            Length 624;
                                                                                                                           Indels
                                                                                                                        70;
                                                                       DB 7;
                                                                                             9.3;
constructed by Yulan Piao."
                                                                                                                   0; Mismatches
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                                                                         Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: custom primer used
High quality sequence stop: 305.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                       153 GACAGAGCGTCCCCTCTCC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2395039"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
/lab_host="DH10B"
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Mus musculus
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                                                                         18.6%;
51.7%;
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                                                                                                                      75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                             Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 624)

Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.

Construction of long-transcript enriched cDNA libraries from submigrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                 CF913548 624 bp mRNA linear EST 05-NOV-2003 B0950D02-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0950D02 IMAGE:30477061 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fnote="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sal1; Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics. National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgum.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Rese 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                   81 CCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTA 140
                                                               clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="NIA:B0950D02 IMAGE:30477061"
dev stage="Unfertilized Egg"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Organism="Mus musculus"
|mol_type="mRNA"
|strain="C57BL/6J"
|db_txef="niaEST:B0950D02-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 11 (9), 1553-1558 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0950 row: D column: 02
Seg primer: M13 Reverse
                                                                                                                 141 TCGCGCCTATAAATACAGCCCGCAA 165
                                                                                                                                                             555 CGCCACGAGGCGCCACAGAGGCAA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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TITLE
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CF913548
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Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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Search completed: May 10, 2005, 07:25:12 Job time : 1244.12 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

May 10, 2005, 03:40:34; Search time 3416.8 Seconds (without alignments) 7998.346 Million cell updates/sec Run on:

US-09-896-888A-1 564

1 catgatgataaacaatgtat.........tgttacagcgacacacatg 564 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4708233 segs, 24227607955 residues Searched:

9416466 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

9b htg.; 49b htg.; 49b on: 49b on: 49b ov: 49b

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

|        |       | æ     |                 |    |            |                                |
|--------|-------|-------|-----------------|----|------------|--------------------------------|
| Result |       | Query |                 |    |            |                                |
| No.    | Score | Match | Match Length DB | ВВ | QI         | Description                    |
| 1      | 564   | 100.0 | 564             | 9  | BD070856   | BD070856 Insect ex             |
| 7      | 564   | 100.0 | 4170            | 14 | NPHTTAA    | M83827 Orqyia pseu             |
| ო      | 564   | 100.0 | 131995          | 14 | OPU75930   | U75930 Ordvia pseu             |
| Ω<br>4 | 562.4 | 99.7  | 1429            | 14 | S64501     | S64501 p8.9=8.9 kd             |
| S      | 548   | 97.2  | 2773            | 9  | AX766573   | AX766573 Sequence              |
| 9      | 111.8 | 19.8  | 118584          | 14 | AY043265   | AY043265 Epiphyas              |
| c 7    | 101.8 | 18.0  | 131526          | 14 | AY145471   | AY145471 Rachiplus             |
| ص<br>ص | 101.4 | 18.0  | 1511            | 14 | NPHPE38    | M62488 Autographa              |
| o<br>0 | 101.4 | 18.0  | 133894          | 9  | A48542     | A48542 Sequence 1              |
| c :10  | 101.4 | 18.0  | 133894          | 14 | L22858     | L22858 Autographa              |
| 11     | 100   | 17.7  | 131158          | 14 | AY327402   | AY327402 Choriston             |
| c 12   | 93.4  | 16.6  | 28413           | 9  | BD187790   | BD187790 A virus i             |
| c 13   | 93.4  | 16.6  | 128413          | 14 | NPHT3 COMP | L33180 Bombyx mori             |
| c 14   | 92.2  | 16.3  | 129609          | 14 | AF512031   | AF512031 Choriston             |
| c 15   | 92    | 16.3  | 2178            | 14 | NPBBMIEN   | D14467 Bombyx mori             |
| 16     | 90.4  | 16.0  | 2011            | 14 | NPHIEN     | M59422 Autographa              |
| 17     | 73.8  | 13.1  | 155060          | 14 | MBU59461   | U59461 Mamestra co             |
| 18     | 72.2  | 12.8  | 4051            | 14 | AF246708   | AF246708 Spodopter             |
| c 19   | 72.2  | 0 00  | 130343          |    | ABOUTHE    | 11 4 1 1 7 1 1 1 C C C C C C C |

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Length 564;

Query Match 100.0%; Score 564; DB 6; Length 5 Best Local Similarity 100.0%; Pred. No. 4e-171; Matches 564; Conservative 0; Mismatches 0; Indels

1. .564
/organism="unidentified"
/mol\_type="genomic DNA"
/db\_xref="taxon:32644"

ORIGIN

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| υ        | 20                   | 72.2       |                              | œ. ۳. ۰    | 153656  | 44.        | AF539999<br>AF107100 | 7100           |                        |               | AA        | AF539999             |                       |   |
|----------|----------------------|------------|------------------------------|------------|---|------------|----------------------|----------------|------------------------|---------------|-----------|----------------------|-----------------------|---|
| C        | 22                   | 68.7       | 2 5                          |            | 158482  | 14         | AY12627<br>AF30304   | 6275<br>3045   |                        |               | AY        | AY126275<br>AF303045 | Mamestra<br>Helicover |   |
| ט        | 24                   | 66.4       |                              | 8          | 14235   | 14         | HZU67264             | 7264           |                        |               | 90        | U67264 F             | a                     | _ |
| U        | 25                   | 65.6       |                              | 9          | 130869  | 14         | AF334030             | 4030           |                        |               | AF        | AF334030             | Helicover             |   |
| υι       | 26                   | 65.4<br>64 |                              | ۰ ۰        | 135611  | 14         | AFIB                 | 1059           |                        |               | A A       | AF169823<br>AF271059 | Spodopter             |   |
| ט        | 78                   | 63.6       |                              | . m        | 161046  | 14         | AF08                 | 1810           |                        |               | AF        | AF081810             |                       |   |
| U        | 29                   | 59.2       |                              | 'n         | 113220  | 14         | APOO                 | 6270           |                        |               | AP        | AP006270             |                       |   |
| ט        | 30                   | 41.8       |                              | 4.         | 131158  | 14         | AY32                 | 7402           |                        |               | AY        | 327402               |                       | _ |
| U (      | 31                   | 40.2       |                              | ٦. ٥       | 128380  | 7          | ACISI                | 600            |                        |               | A S       | 51093                |                       |   |
| טנ       | 2 C                  | 20.0       |                              | 9 0        | 0000  | ט מ        | AXSYBBSY             | ט<br>ה<br>ה    |                        |               | AX2       | AX596859<br>AX551255 | Seguence              |   |
| ט ט      | 3.4                  | 39.6       |                              | 0          | 9289  | o vo       | AX767                | 69             |                        |               | XX XX     | 67469                |                       |   |
| •        | 35                   | 39         |                              | 6          | 152573  | 7          | CR3761               | 337            |                        |               | 8         | 76837                |                       |   |
| O        | 36                   | 39         |                              | ō          | 200989  | 'n         | BX000                | 666            |                        |               | BXO       | 66600                |                       |   |
| ပ        | 37                   | 38         | 9                            | ٠.         | 6289  | 9          | AX599                | 205            |                        |               | AXS       | 99005                |                       |   |
| U        | 8 6                  | 38         |                              | ٠. ۱       | 9289  | φ.         | AX767                | 245            |                        |               | AX7       | 67545                |                       |   |
|          | χ,<br>γ,             | 5          |                              | •          | 160376  | 4 (        | ACIDO                | V .            |                        |               | ACI       | ACISOSIS             | Bos cauru             |   |
| υ        | ) t                  | 37.4       |                              | ب ب        | 105424  | N 0        | AC020                | 384            |                        |               | ACO       | AC020384             | Drosophil             |   |
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| ţ        | 7 7                  |            |                              | j. r       | 190808  | ν <u>-</u> | AC093                | יים מ<br>ה בים |                        |               | A.C.      | AT.028537            | MOLIGE BADI           |   |
| ט כ      | 4 4                  |            | 9 (2                         |            | 221128  | 2 -        | AC12                 | 3846           |                        |               | 4         | AC123846             |                       |   |
| טט       | 45                   | 36.4       | φ                            | 'n         | 505   | 9          | AR4241               | 142            |                        |               | AR4       | AR424142             | Ŋ                     |   |
|          |                      |            |                              |            |   |            | AL                   | IGNM           | ALIGNMENTS             |               |           |                      |                       |   |
| RES      | RESULT 1<br>BD070856 | -          |                              |            |   |            |                      |                |                        | ,             | ;         |                      |                       |   |
| rocas    | :US                  |            | BD070856                     | و          |   |            | ũ                    | 564 bp         |                        | DNA           | linear    | PAT                  | 27-AUG-2002           | ď |
| DEF      | DEFINITION           | z          | Insect e                     | exp        | expression vectors                                | A Ve       | ctors.               |                |                        |               |           |                      |                       |   |
| VER      | VERSION              |            | BD070856                     | 6.1        | GI  | :2261645   | 459                  |                |                        |               |           |                      |                       |   |
| KEY      | KEYWORDS             | ч          | 2001                         | 516        | 5   |            |                      |                |                        |               |           |                      |                       |   |
| nos      | SOURCE<br>ORGANISM   |            | unidentified<br>unidentified | ifi<br>ifi | e d   |            |                      |                |                        |               |           |                      |                       |   |
| •        |                      |            | unclassified                 | ifi        | ed.   |            |                      |                |                        |               |           |                      |                       |   |
| REF      | REFERENCE            | П          | (равев                       | 68         | 1 to 56   | 564)       |                      |                |                        |               |           |                      |                       |   |
| ∢ (      | AUTHORS              | g.         | iglia                        | tt:        | Grigliatti, T.A., Theilmann, D.A.,                | The        | i lmann              | Α.Ο.           | ., Pfei                | Pfeifer, T.A. |           | and Hegedus, D.D     | B, D.D.               |   |
| <b>≒</b> | TUTLE                | 4 6<br>6   | Bect                         | ek<br>F    | Insect expression vectors                         | , ce       |                      | ū              | ייטטר ממט שנ           |               |           |                      |                       |   |
| 5        | OOK                  | THE        | FINI                         | ZER S      | INTVERSITY OF                                     | BR         | ٠ <u>;</u>           |                | COLIMBIA               |               |           |                      |                       |   |
| Ö        | COMMENT              | SO         | ,                            | 111        |   | nuc        | leopol               | hed            | rovirue                | 00            |           |                      |                       |   |
|          |                      | PN         |                              | 20         | JP 2001516225-A/1                                 | 5-A        | /1                   |                |                        |               |           |                      |                       |   |
|          |                      | PD         |                              | -SE        | P-2001  |            |                      |                |                        |               |           |                      |                       |   |
|          |                      | PF         |                              | Ψ¥         | 26-MAR-1998                                       |            | 1998541010           | 1010           |                        |               |           |                      |                       |   |
|          |                      | PR.        | 27                           | ξ,         | R-1997  | SD         | 09                   | 1499           | 60/049946, 28-JAN-1998 | JAN-19        | و<br>ا    | 222                  | 2221819 PI            |   |
|          |                      | 4          | DFETF                        | ب<br>م م   | THOMAS A GRIGLIAITI, DAVE A<br>A PFETFER DWAYNE D | ,<br> <br> | OAVE A               | H              | I LMANN,               | THOMA:        | •         |                      |                       |   |
|          |                      |            | ÄH                           | HEGEDUS    |   | 1          |                      |                |                        |               |           |                      |                       |   |
|          |                      | P.         |                              | 2N1        | C12N15/85, C12N5/06, C12N15/69//C12N9/22          | 2N5        | /06,C13              | 2N15           | /69//CI                | 12N9/2        | ~         |                      |                       |   |
|          |                      | ပ္ပ        |                              | Insect     |   | ssi        | expression vectors   | COLB           |                        |               |           |                      |                       |   |
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|          |                      | 4 1        |                              |            | . ب <b>ن</b>                                      |            | /organi              | המינו          | ='Multi                | icanai        | June 1 Po | polyhe               | drovinia'.            |   |
| FEA      | FEATURES             | •          |                              | ,1         | ocation   | 0/         | ) organ              | 9 9            | 1                      | i cabo        | 1         | 7.7.7                | Location/Onalifiers   |   |
|          | source               | e<br>e     |                              | ı          | 564   |            |                      | ł              |                        |               |           |                      |                       |   |

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SAPRAAPRRVHAVGDPGAPLRASYALPNGVYNLHGDAHFNPPEEDDDI LFVDTAAEQA
RQRAVNLHEAVNRHERLRRELGERMTRSPTLLNYSPSYSPTSPRSRSPDLIMPEDLQP
AREQPLAPFNDSDDDERLLEQVMLESAEAPQLPQAPPAPQVDVSVLCHI CSCTFTDI Q
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TVRDSQAIKRHWAQLSDSNMPHSNEMTTIQELQAELAELRAATARAHHDVNMARSDSQ
LLRQQLDVKEAELAHESNARIKLQKQNETLSANNLSLQHQLNTQVIESRVKMEQFKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /traislation="MSSRYSPYRIRNYGERRRYQERLLSEFNSRPYTAVAAVCAVCLE
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AQKEARDLQESMERQKQAHVVAMNSSCEQYTALQTTLADMQAQLDRSBALSSTLAEHN
RAANVOIDSLERAYQELBAAQSAPVSVNVEFNDNARQNTNLHERFRSYVSTVSDMMI
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/db_xref="GI:332541"
/translation="MSRSNNANAPTPSNRRRNLSLVRGRRLTYSPPDAASAQRASPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF; homologous to the ACMNPV PE-38 gene; putative"
/codon_start=1
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100.0%; Pred. No. 6.1e-171;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                   product="transcriptional trans-activator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /prote<u>in_id="AAA46750.1"</u>
/db_xref="GI:332542"
                                  /gene="IE-2"
/gene="IE-2"
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/gene="IE-2"
691. .1908
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/gene="IE-2"
2017. .2759
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/gene="IE-2"
2944. .>3907
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The limani, D.A. and Stewart, S.
Tandemly repeated sequence at the 3' end of the IB-2 gene of the baculovirus Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus is an enhancer element
Virology 187 (1), 97-106 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orgyia pseudotsugata nuclear polyhedrosis virus transcriptional trans-activator (IE-2) gene, complete cds; ORF, complete cds.
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                                            TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCCACCACCAACTTTTTT
                                                                                                               GCACTGCAAAAAAACTCTATTGCACGGGCCCCATACATAGTACAAACTCTACGTTTC
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                                                                                            GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
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Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Viruses dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.

1 (bases 1 to 4170)

Theilmann, D.A. and Stewart, S.

Molecular analysis of the trans-activating IE-2 gene of seudotsugata multicapsid nuclear polyhedrosis virus
Virology 187 (1), 84-96 (1992)
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|--|---|--|--|--|--|
| SGD  | SGD SGD   | CDS  | CDS  | CDS  | CDS  |
|  | OPU75930  N Orgyia pseudotsugata multicapsid nucleopolyhedrovirus, completed genome. U75930.2 GI:11024985  Orgyia pseudotsugata multicapsid nucleopolyhedrovirus Orgyia pseudotsugata multicapsid nucleopolyhedrovirus N Orgyia pseudotsugata multicapsid nucleopolyhedrovirus N Orgyia pseudotsugata multicapsid nucleopolyhedrovirus I (bases daDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus I (bases 1 to 131995)  | Ahrens, C.H. Rohrmann, G. The sequent polyhedrosi Virology 22 9126251 2 (bases 1   | Intide Direct Submitted (23-0CT-1996) Oregon State University, Agricultural JOURNAL Submitted (23-0CT-1996) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA AUTHORS Rohrmann, G.F. TITLE Direct Submission JOURNAL Submitted (06-MAR-1998) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA REMARK Sequence update by submitter REMARK Sequence update by submitter AUTHORS Rohrmann, G.F.        | TITLE Direct Submission  JOURNAL Submitted (26-OCT-2000) Oregon State University, Agricultural  Chemistry, Corvallis, OR 97331-7301, USA COMMENT Sequence update by submitter  COMMENT On Oct 26, 2000 this sequence version replaced gi:2934903.  FRATURES Location/Qualifiers  1. 131995  source /organism="Orgyia pseudotsugata multicapsid nucleopolyhedrovirus"                   | /mol type="genomic DNA" // Ab xref="genomic DNA" // Ab xref="genomic DNA" // note="gimilar to Autographa californica nuclear // note="gimilar to Autographa californica nuclear // polyhedrosis virus (AcMNPV) deposited in GenBank Accession // Nucle="ORF1; pk-1; similar to AcMNPV ORF10" // complement(123947) // note="ORF1; pk-1; similar to AcMNPV ORF10" // protein id="AAC59000.1" // protein id="AAC59000.1" // brafilation="MDAALQSLRFVDACAVLAPKVVNGRFGKMDVLHHRPTTSKLFL // Arsef="Gi1:1911247" // Ab xref="Gi1:1911247" // |

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Query Match
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9893. .11362
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VALPRINVLAGYKFSOTAVLHKUNVPAPTYQAĞLİQSBEALQARVPMYCLEMMGDÖFHH
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KQQFGKSTPTIRQLRDNVQLLLLINLHPVYDINRPVPPSVQYLGGGLHLAQALPQRLDA
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                                         tyrosine phosphatase 2"
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Wu,X., Stewart,S. and Theilmann,D.A.
Mu,X., Stewart,S. and Theilmann,D.A.
Characterization of an early gene coding for a highly basic 8.9K
protein from the Orgyia pseudotsugata multicapsid nuclear
polyhedrosis virus
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                                                                                                                                                              128172 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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                                                                                                           CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                      TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
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                                                  Indels
; Score 564; DB 14;
; Pred. No. 1.3e-170;
0; Mismatches 0;
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                                                                                                          'note="p220p2F expression vector for insect cells"
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100.0%; Pred. No. 8.6e-166;
ive 0; Mismatches 0;
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2551. .2556
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                                Location/Qualifiers
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99.8%; Pred. No. 1.6e-170;
iive 0; Mismatches 1; Indels 0;
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Sequence 60 from Patent WO03042244.
AX766573.1 GI:32260450
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KEYWORDS
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complement (2717. .3070)
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                                                                                                                                                                                                                                                                                                                                                                                                         complement (2104. .2715)
/gene="lef-2"
complement (1713. .2090)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (3426. .3935)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTTAAEQHTICDKL"
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                                                                           codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="ORF4"
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/note="ORF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="ORF5"
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                                                                                                                                                                                                                                                                                 Epiphyas postvittana nucleopolyhedrovirus, complete genome.
AY043265
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LANIVSRVEHLLRYEIVNDVBITTLSGDFYEEYSKYAARQYALSIQMPPPPPVITPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPLTPHQVPPPPPPPTTPLQGLLPVRDVBATPSPPSTLŠKSTTLDBFPSYSNASMIQ
LPVTPIKPLI PVKPEHLKFKPKTI I SELPDMPATNNLDDQKLPAPPPPPPP PPSPPLL
PSNDLPPPPPPPLLPSGNVPPPPFIEGMLDDMLINAI IAGNNKSEKVNTDARGDMLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKKGVTLKFSKTNKSDKKVDDRADLLNSIKIGVKLKPIKVNTNQPLPEAPVTDISVIA
STLKKRRANI 16QSESSBSNSSQSWDBEGNTQTIRKANKDHLKYAVNLYNFRATTHAY
RTNSELPKLLDNVFSLLDRYSSLSNVBAKNILDNLKERVKLTSNQLDNAEAQSLYI
NDPNQPYIQVBDLIFARRYADAKMHLDLAITESGNDERLRRKKRANDLDAVVV*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHLDPLDHYWVAEDPFLGFGKNQKLTLFKEIRNVKPDTWKLIVWSGKBFLRETWTRF
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VGMNNEYRISLAKKGGCCPINNIHSBYTNSFESFVNRVIWENFYKPIVYIGTDSGEBE
EILIEVSLVPKVKEFAPDAPLFTGPAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein id="AAK85565.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-JUL-2001) Microbiology, University of Otago, PO Box
56, Dunedin, New Zealand
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 118584)
Hyink,O., Dellow,R.A., Olsen,M., Caradoc-Davies,K.M.B., Drake,K.
and Ward,V.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyink, O., Dellow, R.A., Olsen, M., Caradoc-Davies, K.M.B., Drake, K. and Ward, V.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Epiphyas postvittana nucleopolyhedrovirus"
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/note="EpipomRyV"
/note="ORF136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Epiphyas postvittana nucleopolyhedrovirus
Epiphyas postvittana nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete sequence of the Epiphyas postvittana
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'db_xref="GI:15213127"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleopolyhedrovirus genome
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                                                                                                                                                                                                                                                                                                                                                                                                             AY043265.1 GI:15213125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon start=1
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                               548
                                                                                                   545 CATCTGTT 552
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                           541 CATCTGTT
                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
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SOURCE
ORGANISM
                                                                                                                                                                                                                      RESULT 6
AY043265/c
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AUTHORS
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TITLE

TITLE

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114732 CTACGAATCGTAGACTATTTAACTTGAATAGTCTACACTGTTCTATACGCTCCTAATACA 114673
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VKEFTEKCPGMLVGVHCTHGINRTGYMVCRYLMHTLGIAPQEAIDRFEKARGHKIERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="WKLTYKMASLLKYALRLTREYKENIIPHPDHLTRLRDLIDGMIK
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SPDCNKFLRSDDMTPVVTTITPKRTADYKITEYVGDVKTIKPSDRPLVESGPLMREAA
                                                                                                                                                                                                                         circular VRL 07-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rachiplusia ou multiple nucleopolyhedrovirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 131526)
Bonning, B.C. and Harrison, R.L.
Direct Submission
Submitted (JAUG-2002) Entomology, Iowa State University, Ames, Iowa 50011, USA
                                                                                                                                                                                                                            AY145471 131526 bp DNA circular VRL 07-JUI
Rachiplusia ou multiple nucleopolyhedrovirus, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
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join(131515: .131526,1. .326)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harrison, R.L. and Bonning, B.C.
The nucleopolyhedroviruses of Rachiplusia ou and Anagrapha
faloifera are isolates of the same virus
J. Gen. Virol. 80 (Pt 10), 2793-2798 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 131526)
Harrison, R.L. and Bonning, B.C.
Comparative analysis of the genomes of Rachiplusia ou and
Autographa californica multiple nucleopolyhedroviruses
J. Gen. Virol. 84 (Pt 7), 1827-1842 (2003)
                                                                                  114672 CTACTACACATTGAATTTTTTTTGTAGTGCAAAAAATTACATAT 114630
                                                                                                                                                                                                                                                                                                                                                   Rachiplusia ou multiple nucleopolyhedrovirus
Rachiplusia ou multiple nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                      232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTGT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392. .898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (962.
                                                                                                                                                                                                                                                                                                    AY145471.1 GI:23476465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleopolyhedrovirus.
1 (bases 248 to 8029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .131526
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22695336
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
                                                                                                                                                                             RESULT 7
AY145471/c
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JOURNAL
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TITLE
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REFERENCE
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TITLE
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALOLLNPINGNSVSDYHVKPLDEGGREWVIDADFKNYVNKTELMLKINVGATALLLFY
TEMHYHRIMFSGNRGFHMMLKFADGFKIGALKSVREHWYRIFEKPTKINNRDIRALLFY
AHCMQRAVNMYQDQILQSSKPDELILHFWPDVDKDVFCNPTKQIRAPFSYNHKGTQFS
RCITQQLLEKIQKCSTGCSDGGASTSSISNITH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /traislation="MHFAVILILLAAQAHAANILAVLPTPAYSHHLVYKAYVQALANK
CHNVTVIKPQLLNYVDSNAHWCGHIEQIEADMSSEQYKKLVSSSGAFRKRGVVADETT
VTANNYMGLIDMFKDQFNNVNVQQFLLCNRTFDVVVVVBAFADYALVFGHLFRPAPVIQ
IAPGYGLDENFDTAGAVARHPKYYPNIWRSTFVGGTAGALSEWRLYNBFELLARYSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKTLERQLNASVNGIVYVSFGSSIDTKSIHDEFLQMLVNTFTGLANKTVIWKVDDAVV
SIKLDPNYTQNWFNQRAVLHKNYTVAFVTGGELQSSDEALHAQVPMYCLPMMGDQF
HHANKLQEFKVARTITYVDVSSOLILAITDVIVNKTYQTRWAELRAVIDYDEIAPA
DKAIKFTERVIKFGHDITYPARSLKSPAANLDQSNYFISFPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAK85577.1"
/db_xref="G1:15213138"
/translation="METPRAMIPSERATPKRAALGTFVKTVVTTTTVSGRGLTRDERNR
/translation="METPRAFYRAMORLVRKKNNIIADLAAQLERRRCRSKGSK
YFAVICQNGVLITISGSGQFVRQRVANMCAVGGBQIFCERRNDCARDRQLIAEALAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                          /translation="MFDWMFGWWSFNEQHQQHHPLANHFNAQDYKQYAVDRRAQSDLV
NRSVFKCHPFTFKFRYVIDDDNGRCCRVVDFCKGLEINHELMLNCKWDSKHVRHLNEI
                                                                                                                                                                                                                                                KTVLKHIKTLINVNSDKPINAHKLFENQVČARFEQLEQRLETLERVPDAPTMPGVIFPR
DVNKHQHLAVFVNQERGNTQIGFARGQEEYFRKRKLEFEEEDMHKMLETVHPNPQMAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLKIQFGPTTPTIRELRNNVQLLLLLLHPVYDNNRPVPPSVQYLGGGLHLTQTQPQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MDLTITLIPISLKNIEEPKRSECFKLTSMREDAEFCLNVKCRSP"
                                                                                                                                                                                                                              VFKTPPVEISPDSMGTVYATKHGLIQILQQLSFEYKDDVLLAIKTDKGYDCDDVRDNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MATYMYTLDRVNLMWNSIAYNNSRKFAFMTLKQRWIHVDRHFDN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                  QCIKDRFISNGYKIKKVSNRRRVIBVDCNINAAKDIVNNVIIS"
complement (6427. .7182)
/gene="lef-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score Lill,

Pred. No. 4.8e-24;

":-matches 32; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ORP11"
/codon start=1
/product="LBF-1"
/protein id="AAK85575.1"
/db_xref="G1:15213136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAK85578.1"
/db_xref="GI:15213139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="AAK85576.1"
                                                                                                                            /protein_id="AAK85574.1"
/db_xref="G1:15213135"
                         .6490)
                                                                                                                                                                                                                                                                                                                                                                          complement (6427. .7182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="GI:15213137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="unknown"
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/product="unknown"
TVAEAYNNVLKNNII"
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/note="ORF13"
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/note="ORF14"
                                                                                                                                                                                                                                                                                                                                                                                               gene="lef-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7254. .8732
/gene="egt"
7254. .8732
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/gene="egt"
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Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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CDS

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129942
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VLVCKRPSSKYNVIFDSINHQHLKGVYKKTDVQITNYNKYINCICNELRQDEFYAKSS
WIASICCHQRATIFSYTNKQVEMKYHLXNVAIVESEDCNEFYPFEPTSDCLICKQKNQ
COMPALement (B253, 2239)
/note="roll; ac13-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESVLKHVKKLNANSEKFMVTHETFKNEVGNR FEOFELRIHELDAKLINMLOSAEKLKTA
VVTESONGTVTFPRDITKHQHLAVFSERIDDRIKLAFVLGOERHFRKRKMRFEDDMEV
LYDGVHPNPLLAIQCINEKLYDKHYKIRKIAKRVIDVNCTPNVVKEVIQEVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="WTILCWLALLSTLTAVNAANILAVFPTPAYSHHIVYKVYIEALA
EKCHNVTVVKPKLFEYSTKTYCGNITEINADMSVQQYKKLVANSAMFRKRGVVSDTDT
VTAANYLGLIEMFKDQFDNINVRNFIANNQTFDLVVVEAFADYALVFGHLYDPAPVIQ
JEGRQCKDVYKNLKDVFDVLHAHSMSDKDKNSLMDLLCVMDCEEIDVDCFYYIFEAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="late expression factor - 1"
/protein_id="AAN28070.1"
/db_xref="GI:23476523"
/translation="WLLCNYTQKRVDMWWDALAYNDSRKYAFWTVNARWIHADRYFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQLYNY IVQNKVSDVHVKPLDDGGGREWVVDADYKNYVDEHDLMLKI YIGATAFLLF
YEBRVSKWYNYTGNRGFHLMLRFTDFKTITSADVRVHRYKVEKPEKDAKLLDSDY IQPGS
FAHCVREAVRLYVEHIQESNFDALTLQYWPDVDRDIFCIVNNKQIRAPYSYNYKGTKFFS
RCITKELLDKLKQCYPGYGGGGPVTTTATTSSPLKIGLIQTTTKSTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAPCYGLAENFDTVCAVARHPVYHDNIWRNNFDDTEANVMTEMRLYKEFKILANMSNA
LLKQQFGPNTPTIEKLRNKVQLLLINLHPIFDNNRPVPPSVQYLGGGIHLVKNAPSTK
LNPVINAQMNKSKSGTIYVSFGSSIDTKSFANEFLYMLINTFKTLDDYTILWKIDDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKNITLPVNVITONMFNORAVLGHKKMVAFITOGGLOSSDEALEAOIPMICLPMMCDO
PYHAHKLQOLGVARALDTVTVSSDOLTVAINDMLFNAPIYKKHMAELYALINHDKATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MLSWLWNWWMWSSDNDSDDVIAVEDRFNPDDYKKYHINAQOWSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIVFHKPSSKRDLNSLGALFATKHGLLEILMQLNFANKSNALLHIQTEGERDDLRDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MLFTIIYLVFLRGALCGCALSAFINAHQPKQVIIVPGRSKAKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLDKAIKFTERVIRYRHDISRQLYSLKTTAANVPYSNYYMYKSVFSIVMNHLTHF"
11578. .11745
/note="rol3a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130001 AACTTTTTGCAATGCAAAAAGTTCACTTTTGCTCGGCATTCAATATACAATACAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVKWDSFKCNTHTFKYRYVHSDTNAKCYNVIDFCKGLEIAHDDILDCNWDGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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/protein_id="AAN28031.1"
/db_xref="G1:23476484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101.8; DB 1-
Pred. No. 8.6e-21;
0; Mismatches 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(9128. .9931)
/note="lef-1; ro12; ac14-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10045. .11565
/note="egt; rol3; ac15-like"
/codon_start=1
                                                                                                                                                                      protein_id="AAN28100.1"
db_xref="GI:23476553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAN28055.1"
/db_xref="GI:23476508"
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/db_xref="GI:23476614"
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/protein_id="AAN28087.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11711. .12388
/note="rol4; ac16-like"
/codon_start=1
                                                                                    note="ro10; ac12-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                           codon start=1
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77.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="G1:23476546"
/translation="MAVIFNNKQLLADDSIENGGELFLLNGSYSILENYVNPVLLKNG
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ASSLCENKIILSQINCESFENDFKHYLDDYNYAFSIIDNSTNVLVAFGLYC"
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HDSKCVGEVMHLLIKSQDVYKPPNCOKMKNVDKLCPFAGNCKGLNPICNY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SASPPPPPPPPPPPPPPPPPPPPPPPWVDLSSAPLPPPLVDLPSEMLPPPPPPPPPSSCYTTLK
SGTYTLKPACKTPCSEI IPKSS ITDVLADTISKRRVAMAKSSEATSNDEGWDDDNR
SNKANKPDVKYVQSLFNYFTSSQLYTNDNDEKNYKAHDILNDVEALLQNKTGYNIDKA
RLLLQDLASFYTLSRPLDSFYTIGSEKQPLFETNRNLFYKSIEDLIFKFRYKEAENHL
IFALTYHPKDYKFNELLKYVQQLSVNQQRTESSA"
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MSCIERDVTAMRRIKEGSCTFDEAVKMIDACDSIKSLSHWFGTSEWGINDNYREVLE
DIDAVVPVSVVQNGWDIFSLNNKFERSISQDMLDCLQIILGRFEYFRRNGKLIRLSTV
FNDNNNVVGWWYNKFCVYTYVHRINYQSVPAELAPRLSEAVKKFIRLRKSDYDDRLHL
DESYNCPRVIAEIYGRFCGIGKEHFSKHKLSCMHILFQYLRGKTTQEEESFPCYRVIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MPDYSYRPTIGRTYVYDNKYYKNLGSVIKNAKRKKHLIEHEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KHLDPLDNYMVAEDPFLGFGROCKLTLFKEIRNVKPDTMKLIVMSGKEFMRETWTRF
VEDSFPIVMODEVMDVTLVNLRPTRENRCYKFLAQHALRWDEDYVPHEVIRIVERSY
VGMNNEYRISLAKKGGCCPIVMIHSEYTNSFESFVSRVIWENFYKPIVYIGTDSGEEE
EILIEVSLVFKVKEFAPDAPLFTGPAY"
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LQIKGELSYQLVSNIIRQLCEALNDLHKHNFIHNDIKLENVLYFEALDRVYVCDYGLC
KHENSPSVHDGTLEYFSPEKIRHYNYARSFDWYAVGVLTYKLLTGGRHPFEKSEDEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MATTNATLQTLIQFYENCKNVKTRYKIINGRFGKISILSHKPTS"
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                                                                                                            2
                                                                                                      product="late expression factor
protein_id="AAN28095.1"
(db_xref="G1:23476548"
                                                                                                                                                                                                                                                                                                                                         note="orf603; ro5; ac7-like"
codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="protein kinase - 1"
               1756. .2388
/note="lef-2; ro4; ac6-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5624. .6442
/note="pk-1; ro8; ac10-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3230. .3967
/note="polh; ro6; ac8-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3997. .5625)
/note="orf1629; ro7; ac9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="polyhedrin"
'protein_id="AAN28081.1"
'db_xref="G1:23476534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAN28027.1"
/db_xref="GI:23476480"
                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAN28093.1"
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db_xref="GI:23476507"
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db_xref="GI:23476522"
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complement (6515. .7534)
/note="ro9; ac11-like"
                                                                                                                                                                                                                                                                                                                                                                                                     product="unknown"
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132384 AATTTTTTGCAAAGGCAAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT 132325
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Autographa californica nucleopolyhedrovirus clone C6, complete
                                                                                                                                               07-MAR-1997
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Ayres, M.D., Howard, S.C., Kuzio, J., Lopez-Ferber, M. and Possee, R.D.
The complete DNA sequence of Autographa californica nuclear
Virology 202 (2), 586-605 (1994)
94303173

    133894
/organism="Autographa californica nucleopolyhedrovirus"
/mol_type="genomic DNA"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133894;
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Submitted (08-MAR-1999) NCBI, Bethesda, MD 20894, USA
Location/Qualifiers
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Autographa californica nucleopolyhedrovirus
Yiruses; dsDMA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                         166 CTACTACACTATCAACTTTTTTGCATTACAAAAAAGTTCATTTTTGC
                                                                                                                                               linear
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Bishop, D., Possee, R. and Ayres, M.
AUTOGRAPHA CALIFORNICA COMPLETE GENOME SEQUENCE
PATENT: WO 9601320-A 1 18-JAN-1996;
NATURAL ENVIRONMENT RES (GB)
Other publication AU 2897295 960125.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.0%; Score 101.4; 75.4%; Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                       1. .133894
/organism="unidentified"
                                                                                                                                               A48542
Sequence 1 from Patent W09601320
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/db_xref="taxon:32644"
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                                                                                                                                                                                                    A48542.1 GI:2302312
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unidentified
unclassified.
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Matches 126; Conserv
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M62488.1 GI:332470
major early protein PE-38.
Autographa californica mucleopolyhedrovirus
Autographa californica mucleopolyhedrovirus
Autographa californica mucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
1 (bases 1 to 1511)
Krappa,R. and Knebel-Morsdorf,D.
Krappa,R. and Knebel-Morsdorf,D.
Identification of the very early transcribed baculovirus gene PE-38
91101290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mprdtnnrhrstpyerptledlerolodnldsinrrdrwoeroe
enlryovrrroronglesiomeoormmaelnnepvinfkfecsvcletysoosndtcp
fliptycdhgpcpkcytinlosnamiphstyccplcmtoyrmrslkpnavytckfyk
ktoryppydpyrniikvlossydnystyckfyk
byoasbrrolieblygriikologlobloyrtlypocgitynnocigredrys
slvystiselpienryhsionyyyagtsaasscdvnytvnegfen"
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early
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      californica nucleopolyhedrovirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTTTTTTGCAATGCAAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.0%; Score 101.4; DB 14; Length 1511; Best Local Similarity 75.4%; Pred. No. 4.4e-21; Matches 126; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                   VRL
                                                                                                                                                                                                  Autographa californica nuclear polyhedrosis virus major
protein (PE-38) gene, complete cds.
                                                                                        129881 CTACTACACTATCAACTTTTTTGCATTACAAAAAGTTCAT 129841
                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="immediate-early protein PE-38"
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                                                        CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGT
                                                                                                                                                                                   DNA
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/db_xref="G1:332471"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Autographa ca
/mol_type="genomic DNA"
/db_xref="taxon:46015"
complement(1, 294)
                                                                                                                                                                                   1511 bp
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/gene="TE-N"
352. 1453
/gene="PE-38"
352. 357
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379. .1453
/gene="PE-38"
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/gene="PE-38"
1433. .1438
/gene="PE-38"
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                    129941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                    DEFINITION
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                                                                                                                                               RESULT 8
NPHPE38/c
                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
MEDLINE
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KEYWORDS
SOURCE
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MEDSPELVNDGEWANDVELVNANREPERPRIKKINVEPTHKLIVVGWKGKEEFTRETHTERE
MEDSPELVNDGEWANDVELVNANREPERPRIKKYEPTAGHALRCDPDYVPHDVIRIVEPSW
VGSNNEYRISLAKKGGGCPINNLHSEYTNSFEQFIDRVIWENFYKPIVYIGTDSAEEE
BILLENGYLFRVAKEAPDAPLETGRAY"

GOMD-Gement (5287. . 6918)

/ note="synonym: Acorf-9; Ac-61K; Ac-vp78"

/ complement (5287. . 6918)

/ gene="synonym: Acorf-9; Ac-61K; Ac-vp78"

/ note="synonym: Acorf-9; Ac-61K; Ac-vp78"

/ note="synonym: Acorf-9; Ac-61K; Ac-vp78"

/ pene="synonym: Acorf-9; Ac-61K; Ac-vp78"

/ pene="synonym: Acorf-9; Ac-61K; Ac-vp78; required for virus replication; 60713 Da

primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MANASYNVWSPLIRASCLDKKATVLIDPDDFIDKLTLTPYTVFY
NGGYJVKISGLRLYMLLTAPPTINETKNSNFKRSKRNICMKECVEGKRKNVDMLNNK
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HDSKCVGEWHILLIKSQDVYKPPNCQKMKTVDKLCFFAGNCKGLNPICNY"
complement (3759, ,4364)
/gene="Ac-ORF603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MAVIFNNKQLLADNSIEKGGELFLFNGSYNILESYVNPVLLKNG
YLELERAAYAGNILYKTDDFKFIDYINLIKATHSELPEBNGYVNYRKTWRSGTIH
YIKKDIYIYDNKKFTLYDRY IYGYDNNYVNFYERKNEKEKEYEEEDDKASSLCENKII
LSQINCESFENDFKYYLSDYNYAFSIIDNTTNVLVAFGLYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLYNTIAYIERLANIGTVNDSEITMLIADFYDLYSNYNIELPPPQALPRSRRPSVVQP
APAAPUTVIVRGYREQI IRAAPPPPSBYVONI PAPPPPPPPPBMSBLEDPAPPWRTED
QPAAPLODRQQLLERI RNEKNRTRLRPVKPKTAAPETGTI VEVPTVLPKETFEBKEPPSA
SPPPPPPPPPPPPPPPPPPPLVDLSSAPPPPLVDLPSEMLPPPAPSLSNVLSEILKSGT
        SFDCNKFLRSDDMTPVVTTITPKRTADYKITEYVGDVKTIKPSNRPLVESGPLVREAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="major occlusion body protein"
protein.id="AAA66688.1"
db_xref="GI:559077"
/translation="MPDYSYRPTIGRTYVYDMKYYKNLGAVIKNAKRKKHFAEHEIEE
/translation="MPDYSYRPTIGRTYVYDMKYYKNLGAVIKNAKRKKHFAEHEIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mynrryesvosylennrnnkidahoffervdtaeaqiiknniyd
nyvvlanrdyllnilklandyfdnkaymyvddsevsrhynavvkmkrlyigvrdfelro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRLKPAQKRPQSEIIPKSSTTNLIADVLADTINRRRVAMAKSSSEATSNDEGWDDDDN
RPNKANTPDVKYVQALFNVFTSSQLYTNDSDERNTKAHNILNDVEPLLQNKTQTNIDK
ARLLLQDLASFVALSENPLDSPAIGSEKQPLFETNRNLFYKSIEDLIFKFRYKDAENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="polyhedrin; 28642 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: AcOrf-7"
complement(3759. 4364)
/gene="Ac-ORFG03 peptide; 23612 Da primary translation
                                                                                                                                                                                                                                                                                                   note="LEF2; 23926 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Ac-pk-1"
/note="PK1; 31978 Da primary translation product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="viral capsid associated protein"
/protein_id="AAA66639.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIFALTYHPKDYKFNELLKYVQQLSVNQQRTESSA"
                                                                                                                                                                                                                                                                                                                                          'codon_start=1
'product="late expression factor 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Ac-pk-1"
/note="synonym: AcOrf-10"
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db_xref="GI:559075"
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/db_xref="G1:559076"
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1520. .5257
                                                                                                                                                                       note="synonym: AcOrf-6"
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                                                                                 3089. .3721
/gene="Ac-lef2"
                                                                                                                                                                                                             3089. .3721
/gene="Ac-lef2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="Ac-PH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAA66631.1"
/db_xref="G1:559070"
/tb_xref="G1:559070"
/tb_xref="Index one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep-archive one-weep
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DKAIRVHVDNKYKSLFEQTIQNGGFTSNSVVKRGDPLYLQPHTVLITKSGVIQLIMKS
KLPALELQEWLLEEVIPQVLCTGKYDPAIKQREEESKQLVTKLIAFFFFHTNALQAV
VAQKTEELVKKGEFIENIVAIKOKQIEAKDLQVTRVWTDLTMYTGFQETMQKKDEN
OKKDAQVTDLVAKVVDLSDRAVOYPADKRKHPVLCVTRGGTFFTAITGQKTYVENQKH
KRNINVANIVVENIRPNFTVDWNNATDRLQAKRSKRSIVLVRWKKRNNLKIG"
complement (2084. . 2245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKLTYKMASLLKYALRLTREYKENIIPHFDHLTRLRDLIDGMIK
SEDVQRFNRTNRNDLISACMQINVRTYMPNATIDMRKQPNCIYFRICQYCHLEADVPS
PDDHSVYRYLCVACGTPLVIDHPLDVFGHTEEGVNELLEVQRVNAGGEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="MQIKTVLLAFAMFAALNAQHVLAACAETGAVCVHNDECCSGACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MYRTSRINNAPVVASQHDYDRDQIKRELNSLRRNVHDLCTRSGT"
                                                                                                                                             /note="5 Copies of 30 bp imperfect palindromic sequence;
the EcoXI site in the first palindrome is at residue 1 of
the linearized genome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="PTP; 19288 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="BRO; 37769 Da primary translation product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2295. .2750)
/gene="AcOrf-4"
/note="17577 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="AcOrf-5"
note="12435 Da primary translation product"
                                                                                                                                                                                                                                                                                               function="enhancer; replication origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="protein tyrosine phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="baculovirus repeated ORF"
protein_id="AAA6632.1"
db_xref="G1:559071"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="conotoxin-like peptide"
/db_xref="taxon:46015"
/clone="C6"
join(133883. .133894,1. .445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="Acorf-5 peptide"
protein_id="AAA66635.1"
db_xref="GI:559074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="AcOrf-4 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonym: AcOrf-3"
complement(2084. 2245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: AcOrf-1"
503. 1009
/gene="Ac-ptp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: AcOrf-2"
complement(1041. .2027)
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/db_xref="GI:559072"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein id="AAA66634.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1041. .2027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (2295. .2750)
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                                                                                                                                                                                                                                                                                                                         /rpt_type=dispersed
503. .1009
                                                                                                                                standard_name="hr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="AcOrf-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="Acorf-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="Ac-ctx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="Ac-bro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="Ac-bro"
                                                                                                                                                                                                                                                                                                                                                                                                                   gene="Ac-ptp"
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CDS

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/trānslation="MDNYSYRPTIGRTYVYDNKYYKNLGSVIKNAKRKKHLLEHEEDE
KHLDPLDHYNVAEDPFLGPGKNQKLTLFKEIRNVKEDTWKLIVWAGGEEFLEETWTRF
KHLDPLDHYNVAEDPFLGPGKNQKLTLFKEIRNVKEDTWKLIVWAGGEEFLEETWTRF
VGRNNEYR ISLAKKGGGCPIRNIHESYTNSFESFVNRVIWENFYKPIVYIGTDSGEEE
EILIEVSLVPKVKGFPADAPLFTGPAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTVKLINRATLLDLLKLALAENTYADTAYMQVNTTESSRHFATLMRMRNLLLINVQDEHFRN
VLASTVARTENLLRSDAVNDVETTVLSGDFYEEYSRYATRQYVSTDTLPPPPPLTPPT
PETTQAFVADSPPPAQAFVAPSPPPAQAFVAPSPPPAQAFTAPSPQPTFVAPPSPPT
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kqietsckkkkqaeeraesaalkryelaadrmamqakaapycaddgrwstlsqqqled
idrnkeiydriyklqlkqdcllinnknaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="viral capsid associated protein"
|protein | de="AAQ91'783.1"
|db_xref="GI:3749384"
|/translation="wDRQYQSVKSYLNNNNAHNAIDADAFFQLVAGPEAHNLKRGLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canada
On or before Oct 8, 2003 this sequence version replaced gi:1117788, gi:2581770, gi:1754838, gi:4092491.
Location/Qualifiers
1. .131158
                                                                                                                                                                                                                                                                          4 (bases 1 to 131158)
Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.M.
Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lauzon, H.A.M., Jamieson, P.B., Krell, P.J. and Arif, B.M.
Direct Submission
Submitted (10-JUN-2003) Molecular Virology, Great Lakes Forestry
Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario PGA 2ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                      1 (bases 80268 to 81693)
Li,X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and Arif,Bu.M.
Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV
J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Choristoneura fumiferana defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="ORF 149; 1629 capsid Op2/Ac9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:74660"
join(129349. .131158,1. .20)
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/codon_start=1
Virus Genes 13 (3), 229-237 (1996)
97187920
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/protein_id="AAQ91696.1"
/db_xref="GI:37499297"
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/db_xref="GI:37499343"
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/codon off-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleopolyhedrovirus"
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/product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132324 CTACAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACGATACGCTCCCAATATA 132265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 11500 to 13512)
Barrett,JW., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura fumiferana J.Gen. virol. 76 (Pt 10), 2447-2456 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The putative LBF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to eukaryotic primases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIDAVVPSVRVQNGWQI FSLINNFEREI SQDMLDCLQI ILGRFEYFMRNGKLLRI ANV 
PRDNDUVQHWYNKFCVYTYNRI NTRSQPAELTVPRLSGRAVKGRTRLKSDYDDRLHV 
DESYNCPRVI AEMYGRFCGI GKEHFSKHKL,SCMHI LFQYLRGKTTQERKS FPQYRVIR 
DFGRQCKDVYKNLKDVFDLLHAHSNSDKDKNSLMDLLCVMDCEEI DVDCFYY I FESFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MSLAAKLIINNYAKYNEVHDVYGESYHHYRIVQEYLSESYVNG
MSCIERDVTAMRRLKSGSCTFDEAVKMIDAGDSIKSLSHWPSTSETMGIDDNVREVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                           /translation="MATTNATLQTLVQFYENCKNVKTRYKIINGRFGKISILSHKPTS
                                                                                                KLYLQKT I SAHNFNADE I KVHQLMSDHPNF I KI YFNHGS INNQVI VMDY I DCPDLFFT
LQI KGELSYQLVSN I I RQLCBALNDLHKHNF I HND I KLENVLYFEALDRVYVCDYGLC
                                                                                                                                                  KHENSLSVHDGTLEYFSPEKIRHTTMHVSFDWYAVGVLTYKLLTGGRHPFEKSEDEML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CEDEFNPV)
                                                                                                                                                                                                                                             /note="2 copies of 30 bp imperfect palindromic sequence" /function="enhancer; replication origin"
                                                                                                                                                                         DINSMKRRQQYNDIGVLKHVRNVNARDFVYCLTRYNIDCRLTNYKQIIKHEFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choristoneura fumiferana defective nucleopolyhedrovirus complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101.4; DB 14; Length 133894; Pred. No. 1.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132264 CTACTACACTATCAACTTTTTTTCATTACAAAAAACTTCATTTTTGC 132218
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Choristoneura fumiferana defective nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                             complement(7899. .8921)
/gene="AcOrf-11"
/note="40093 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="AcOrf-11 peptide"
/protein_id="AAA66641.1"
/db_xref="GI:559080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                          'protein_id="AAA66640.1"
'db_xref="G1:559079"
                                                                                                                                                                                                                                                                                                  /rpt_type=dispersed
complement (7899. .8921)
/gene="AcOrf-11"
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75.4%;
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Matches 126; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="actin rearrangement inducing factor"
/protein_id="AAQ91678.1"
/db_xref="G1:37493279"
/translation="MLAQINYILQLVLHAALYTITLIAFVFSLMGTINYKYAFLLELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVCWTLFVVFQPQIYKNGHVPVLDARYRDYDRNSLCWSNIVSDTYEVHDTNAIRTDFN
CVYRHDFVKKCVGCRMEVRHDEPTVFNQNQCALIMMVMMTAVLQFWNMYVQRKEMRYK
PTPVKTLYFESAPLKEQDTADEEEEQQSSFRMLEIISEPRVQFQFPESSSLDRLSSPP
                                                                                                                                                                                               DPGASYFFVGEGDTYVVNGHKLAVGGYCTTNSVPRDCNRETSVVLMSLNQWTC1AEDP
RYFAGTSNWTQLAGRQHFDR1LPGQSDRNVLFDRLLGREVNVATNTFRRSWDELLEDG
                                                                                                                                                                                                                                                    TRRFEMRCNARDINNNÄLMFVNPLNPLECLPNVCTNVNYVHTSVRPNFETGECDCGDEA
VTRVRHVVPGDRSSVCASIVDGLDTTTASHRPRVECVNTYTSIGNFSNNKLLCPSDTF
DSNTDAAFAFEVPGSYPLSGNGLDEPTHRFFLDTRSRIRYNDVRGLIN"
                                                                                                                                    /translation="MYRILIVLFLFALLYIVVWPFYQAYQHIQTAQHDYNDTLTDRMD
YIBSVMRRRHYVPMEALPSVQFDTNLGTLAGETLKCMSVPLYVTBIDLPFFDCTQVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNGHSVINLSVLTAFLLGPCVFTTTTWAIYKFLLCYKRAEMHSNFYMKTIISLAHVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT 17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF 10-JUL-2001 JP 2001209305
PI WONKYUNG KANG, NORIKO IMAI, SUMIKO GOMI, SHOGO MATSUMOTO PC C12N15/09, A01K67/033, C12N17/04
CC From 100, 001 to 128,413 of BmNPV genome DNA FH Key 1. .28413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      выву790 28413 bp DNA linear PAT 17-JUI
A virus in which a gene for controlling an insect behavior is
deficient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an insect behavior is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIVQSSSSPNSPDSGIDYDIPQPFYSVPNKVVCKYLCRTHATLCA"
complement (9013, 9327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125657 ACTACCACACACCACTTTTTTGCACTGCAATAAAGTTC 125696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 28413)
Kang, W., Idai, N., Gomi, S. and Matsumoto, S.
A virus in which a gene for controlling an inserpatent: JP 2003024062-A 3 28-JAN-2003;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH OS Bombyx mori nucleopolyhedrovirus
DP 2003024062-A/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 ACTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTAC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB 14;
Pred. No. 3.3e-20;
                                                                                                                                                                                                                                                                                                                                                                       'note="ORF 11; arif Op19/Ac21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF 12; Op18/Ac19"
note="ORF 10; Op20/Ac20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="unknown"
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/db_xref="GI:37499354"
                                                                               /protein_id="AAQ91663.1"
/db_xref="GI:37499264"
                                                          'product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (9013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%;
80.6%;
                                                                                                                                                                                                                                                                                                                                             7898. .8863
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Best Local Simi
Matches 129;
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ORGANISM
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VERSION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
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                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="unknown"
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/db.xref="G1:374998738"
/translation="MASARFIRESLRVTQGFKENIVADITHLARLRALIDGKVTHTDV
HRFGFLDRNALVBAGVANNVQVYPDGTIRLNPKTIYFRVCQKCHAVADVPADDHSI
ARYLCAACGMVLVIDHPLDVFGDTEEGVNELIEVQRINAGGDL"
                 /db_xref="d1:3749917"
/translation="MOSAWWPAAGYSSLQNSEKYLIDPNDFVGVLALSPCTVFKQGL
FRAMSGLELALION="MOSAWWPAAGYSSLQNSEKYLIDPNDFVGVLALSPCTVFKQGL
FRAMSGLELALLTAPKFTFFFKTAFRFFKAYLHRSKRNVCLKACADGSVNLAKALNSLRNPLCN
VKIMMELNNAAPRGGYRKRRPFFTCYLGNVVSCTKCKSACLIGALLHFYKMDFKCVG
EVTHLLIKAEDVYKPSNCAKWKTVNKLCPKAGMCKGKNPICNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / rainslation="MAQIKIGGFKFGEDVFTLRYVLDRDIVKFVAKDVASSLKXNICD KAIRTHVDDKYKTSFEQTIQLGGSTSTNLVKRGDPLYLQPHTVLITKSGVIQLIMKSK LDFAVELQEWILEEVIPOVLCTGKYNPAIKQODENKQLINKUKTFSDHTNTLGTAL LDFAVELQEWILEEVIPOVLCTGKYNPAIKQODENKQLINRWYGFFSDHTNTLGTAL QKTQELVKKQEFIERIVATKOKOFPERADLGVTRVMTDLNRWYGFGTTPROMOKLER RNLSAADIVARVIDLSGRAVQYPEDERKHPVLCVTRGCTFFTALAGGKAYVHNQKLK RNLSAADIVARVIDLDSGRAVQYPEDERKHPVLCVTRGTTFTALAGGKAYVHNQKLK RNLSAADIVARTTRPNPTVDWNNATHRLAAKKSKRTISFDSEQDAQQPATRIKQLLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MYDANQIDENLFVGGYYGNNEAMLQFIKKHDIESVISLIDSDVG
PIRQALGLPAGYHIHVYCEDEPTCMALINAMDALYDYIERRINEGKKILIHCHAGVSR
SATLAVYYWKKWQVSYEKALRFVNNKRNVALSDHFVRFLSSRCTYRFVNNKLKIHVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6450. .6723
/note="4 copies of a 30 bp imperfect palindromic sequence; location similar to Ac hrla"
/function="enhancer; replication origin"
complement (6723. .7871)
                                                                                                                                                                                                                                                                                                                                       /translation="MNRPMMRTANAPVIVSNHDYDREQIRRDLNSLRRSVHELCTRST
IGFDCNRILELSSSSNDVITKSPVIIKNSAATVGQSALVCDKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mepgrminyttcgkviegtnlicekvplkoevfeyvtndedrwt
vsnlvnroralgavidltntlryydgakvrdagvlykkirvpqoevpnedivoeffds
voefsarcpgmligvhcthglnrtgylvcryiidklhvsptdaiarfeaarghkierr
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BUGTARLETRGASRVQAFFALDSLEPPPMMTOSLQVLMGRFWHEVROFALTHYANVF
BPTIKLDGWWYNKFCVLTWYR IIRGTVPABELITRLQAVVTKXIKBYDESNAALAMG
DVYGRFCGIGKDHFAQHKMRSVYIFFQYMRGEVTYADBRFPCFSVIKDFGRQCKETYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MSLCSQLLVYAYYGEYNMPHERYSESYHLYRIVNEYLINSYANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQLQVDILHSHAMTDKQKNALFDLLCCNNASDIDVDCYDYIVKKFYNIAVY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="protein tyrosine phosphatase 2"
protein id="AAQ91731.1"
'db xref="GI:37499332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="protein tyrosine phosphatase 1"
protein id="AAQ91726.1"
db_xref="GI:37499327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="baculovirus repeated ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4155. .4676)
/note="ORF 8; ptp-1 Op10/Ac1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3686. .4168)
/note="ORF 7; ptp-2 Op9"
/codon_start=1
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protein_id="AAQ91675.1"
'db_xref="GI:37499276"
                                                                                                                                                                                                                                                                               protein_id="AAQ91760.1"
db_xref="GI:37499361"
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db_xref="G1:37499275"
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/note="ORF 9; Op11/Ac11"
                                                                                                                                                            complement (1861. .2124)
/note="ORF 4; Op7/Ac5"
/codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                         note="ORF 5; Op8/Ac4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2647. .3657
/note="ORF 6; bro Ac2"
                                                                                                                                                                                                                                                       product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon start=1
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CDS

CDS

CDS

CDS

7;

170

230

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/gene="lef-1"
/note="31098 Da primary translation product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNKHLQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 22231 AATTTTTTGCAATACAAAAAGTTCGCCTATGTTTGACATATAATATACAGTACGAACT 22172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPHT13COMP 128413 bp DNA circular VRL 05-MAY-1999
Bombyx mori nuclear polyhedrosis virus isolate T3, complete genome.
L33180
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Gomi,S., Majima,K. and Maeda,S.
Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus J. Gen. Virol. 80 (Pt 5), 1323-1337 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                        231
Location/Qualifiers
1. .28413
And The more and the more of the mode                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-ocr-1998) Laboratory of Molecular Entomology and Baculovirology, The Institute of Physical and Chemical Research (RIKEN), Hirosawa 2-1, Wako 351-0198, Japan Sequence update by submitter on Oct 14, 1998 this sequence version replaced gi:1196668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (19-MAX-1994) Department of Entomology, University of
California, Davis, CA 95616, USA
4 (bases 1 to 128413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 128413)
Kamiteh.SG. and Maeda.S.
Sequencing of the putative DNA helicase-encoding gene of the legin nuclear polyhedrosis virus and fine-mapping of a region involved in host range expansion (Gene 190 (1), 173-179 (1997)
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 28413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACCACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGGCGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bombyx mori nucleopolyhedrovirus"
/mol type="genomic DNA"
/isolate="T3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="28817 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bombyx mori nucleopolyhedrovirus
Bombyx mori nucleopolyhedrovirus
Viruses; dBDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                           46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="Polyhedrin=PH=AcMNPV orf8"
                                                                                                                                                                                                                                                               Score 93.4; DB 6;
Pred. No. 3.2e-18;
                                                                                                                                                                                                                                                                                                                        0; Mismatches
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1. .738
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                                                                                                                                                                                                                                                            Query Match 16.6%;
Best Local Similarity 72.5%;
Matches 121; Conservative
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SLYNTIAYIERLLNIGTVNDSEITMLIADFYDLYSNYNIELPPPPPQALPRSRRPSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPAAPAPVPTTVHEQTKFEQTTPAAPPPSSVPNIPAPPPPPPPPPPSSMSELPPAPP
MPTKPQPAAPLDDRQQLLEAIRNEKRRTRLRPVKPKTAPETNTIIEVPTTVLPKEPKP
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NNRPNAPDVKYVQALFNVFTSQLYTNDSDEKNTKAHNILMDVESLLQNKTQTNIDKA
RLLLQQLASRVVLSSPRLDSPAIGLQKQPLETNRNLFYKSIEDLIFKFRYKDAENHL
IFALTYHPKDYKFNEILLKYVQQLSVNQQRTESNA"
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GLCKHRNLPSVHDGTLEFFPRETRHNYARSFDWYAVGVLTYKLITGGRHPFEKSED
EMLDINSMKRRQOYNDIGYLKHVRNYNARDFYYCLTRYNLDCRLTNYKQIIKHEFLS
complement (3248. .4270)
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FNPNSDAVGWWYNKFCVITYVHRIMHRSVPAELVPRLSEAVKKFIRLSKSDYDDRLHV
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HLNEIIFHKQKSKRDLNSLGALFATKQGLLKILMRLNFDNKSNALLHLQTEGERDDLR
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KTAIVTESKNGTVTF PRDITKHQHLAI FSERIDDRIKLAFVLGQERHFRKRKMR FEDD
MEVLYDGVHDNPLLAIQCINEKLYDKHYKIRKIAKRVIDVDCTHNVVKEVIQEVL"
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DFGRQCI DVYRDLKDVFDLLHAHSMSDKDSKNSLMDLLCVMDCEEI DVDCFYY I FESFL
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/note="32442 Da primary translation product"
                                                                                                                                                                                                                              EILIEVSLVFKIKEFAPDAPLFTGPAY"
complement (768. 2336)
/gene="orfil629"
complement (768. 2396)
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/forne="orfil629"
/forne="orfil629"
/codoo_start=1
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/note="39756 Da primary translation product"
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/note="393]5 Da primary translation product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="Orf1629=pp78/83=AcMNPV orf9"
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/db_xref="GI:3745840"
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/product="AcMNPV orf11"
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complement(3248. .4270)
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complement (4605. .5600)
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YTERNVSKWYTGNRGPHUMKFTDFKTITSAQNYRVHRYKAFEKPALDSOTQPGS
YTERNVSKWYI PHAMQDSNLDALTLQYWPDVDRDIFCNVNKQIRAPYSYNKGTKFF
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IAPGYGLAENFDTVGAVARHPVHPNIWRNNFDDTKANLMTEMRLYKEFKILANMSNA
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VKNITLPANVITQNWFNQRAVLRHKKMAAFITQGGLQSSDEALRAGIPMVCLPMMGDQ
FYHAHKLQQLGVARALDTVTVSSDQLLLAINDVLFNASTYKKHMAELYALINNDKATF
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LESAPKKYTTTHRNISSKPAAHWKYFGVVCDNTIRTIIGNBERVRRLAELCTLYNA
EYVFCQARADGDKDRQALASLLITAAFGPRVIVYENSRRFEFINPDEIASGKRLIIKHL
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="57044 Da primary translation product"
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/gene="Orf 7a"
/gene="Orf 7a"
/gene="Orf 7a"
/note="6233 Da primary translation product"
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product="LEF-1=AcMNPV orf14"
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/db_xref="GI:3745844"
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complement (9387. .10457)
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8067. .8756
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/gene="Orf_9"
8725. .9357
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'gene="egt"
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DLTDWTLYKEQNETITNFVKKTLIDISGPDLGCRKLMRIYLNTDFRGQLPAYLTHYWN
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Oiu,W., Liu,J.J. and Carstens,E.B.
Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene
expression in insect cells
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Xie,W.D., Arif.B., Dobos,P. and Krell,P.J.
Identification and analysis of a putative origin of DNA replication in the Choristoneura fumiferana multinucleocapsid nuclear
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: nuclear polyhedrosis
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Choristoneura fumiferana MNRV polyhedrin, complete genome.
AF512031 AF177329 S78506 S81690 U10441 U18677 U26676 U26734 U53854
U57401 U59008 U70432 U72240 X65395 S46001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identification, localization, transcription, and sequence analysis of the Choristoneura fumiferana nuclear polyhedrosis virus DNA
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                                                                                                                                                                                                                                                                                      CTACGTTTCGTAGACTATTTTACATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                             Gaps
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 129609)
Lee,H.Y., Arif,B., Dobos,P. and Krell,P.
Identification of bent DNA and ARS fragments
                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                Score 93.4; DB 14
Pred. No. 4.5e-18;
); Mismatches 46
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                                                                                                                                                     YPHKNLCDQNWKRFMSCIFSLY"
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Virology 209 (2), 409-419 (1995)
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VTHILIKAENTYKPSNCAKMKAVTKLCPKANMCKGLNPICNY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MPNFVKFSLRLTRESKENIVAHIGHLSRVRELIDRNVTPADVRR
FRPPDRDALLAACMVVNVQAYGADGTIRLQPTLIYYRVCRNFRAVADVPAPDDHFIAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein id="AAP29801.1"
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VDRVYTNFHSHKNRMVYGQLYSFALSNFSLANQIYIGAPIFEKERMVSVITARHEDYK
NKLVIYPVTGISARGLVSGQINFDLQILTQKLLEGSSVYGKMQLPYKALKDYAISTNR
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SAALVVYYYMSRQMSYEEALSLVKNKRRVAISNHFVRFLASKCSYKFVNNVLKIRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="protein tyrosine phosphatase 1"
protein id="AAP29803.1"

Ab_xref="GI:305987"

/translation="MFPDRWHEFTPCGRVIDGTRLICFKVPLSAELFEYVTNDEDRWT
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VDEFQDRCPTMLVGVHCTHGLNRSGYLVCRYMVDKLGVSPADAIIRFEARGHKIERA
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GQWSKLTSAQLDEI AREKDI VDRI YQLQLKQDRLI KMDGLKKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation="MTRPTMRNAAAVAADYDREQLRRDLNSLRRSVHELCTRSTTGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKNLFKGLPRNVAVFYNERDITIALVEGEFEIDRIRLSGPLILRNIKQQº
complement (3738. .4220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="ORF8; ptp2; Op9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF9; ptp1; Ac1/Op10"
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/note="ORF7; Ac136/Op132"
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/note="ORF4; Ac5/Op7"
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                                                                                                                                                                                                                                                                                                                                                                                   'product="unknown"
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/note="ORF6;Ac2"
                                                                                                       codon_start=1
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Identification and molecular characterization of the Choristoneura funiferana multicapsid nucleopolyhedrovirus genomic region encoding the regulatory genes pkip, p47, lef-12, and gta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MPDYSYRPTIGRTYVYDNKYYROLGSVIRKRKRKHLLEHEEDEK
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GMNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVYIGTDSGEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (13-MAY-2004) Department of Microbiology, University of
Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-MAY-2002) Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                        Identification, molecular cloning, and transcription analysis of the Choristoneura fumiferana nuclear polyhedrosis virus spindle-like protein gene Virology 223 (2), 396-400 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carstens, B.B., Liu, J.J. and Dominy, C.
Identification and molecular characterization of the baculovirus
CfMNPV early genes: ie-1, ie-2 and pe38
Virus Res. 83 (1-2), 13-30 (2002)
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de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
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de Jong, J. G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B.
and Krell, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B. and Krell,P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence update by submitter
On May 13, 2004 this sequence version replaced gi:30269978.
Location/Qualifiers
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    129609
    organism="Choristoneura fumiferana MNPV"

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/protein_id="AAP29795.1"
/db_xref="G1:30269979"
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/protein_id="AAP29796.1"
/db_xref="G1:30269980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:208973"
  217 (2), 564-572 (1996)
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/note="ORF2; Op5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1. .735)
/note="ORF1; Ac8/Op3"
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ORIGIN
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Best Local Simi
Matches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arbemikn 2178 bp DNA linear VRL 03-FEB-1999 Bombyx mori nuclear polyhedrosis virus genes for BmIE-N and BmPE36, partial cds and complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (18-FEB-1993) Gentaro Yamamoto, Nagoya University Faculty
of Agriculture, Dept. of Agricultural Chemistry; Nagoya, Aichi
464-01, Japan (Tel:052-781-5111(ex.6238), Fax:052-781-4447)
Submitted (18-FEB-1993) to DDBJ by:
                                /trānslation="MHSVRNLFDSNMSLSSKLLVYAYYGAFNLLHEKYGESYHLYRIV
HEHLTETYVSNASCVRRDIATARCFENGFCFNLARQLLDVTDVAARLAAWYNRGDKTG
LCANVQLALABIDKYAPLEKRVSIGNNIFALDTIADIPSNALDDFQTIIYEGFKDFVD
                                                                                                                                                 MNNLAHVADVFDPDEKIKAEGWWYYKECVLTYMHRLTVNAVPTELMTRLQDAVIKFVQ
PQNKGNCAPAMANVYGRFCGIGRKHFSQHKAASMYILFQYMRNNLTPKDERHPSFGVI
KDFGRLCKETYTDLRAEADLLYINATTDEKKNALFDLLCCVNAADLDVDCYDYIVDNF
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/db_xref="G1:222185"
/db_x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AACTITITITGCACTGCAAAAAACACGCTTTTGCACGCGGGCCCAIACAIAGTACAAACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Length 129609;
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1 (bases 1 to 2178)
Yamamoto, G. and Kobayashi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124772 CTACCACGTAATGTACATTTTTGCACTGCAAAAAAGT 124736
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                                                                                                                                                                                                                                                                                                                                                                                       Score 92.2; DB 14;
Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BmIE-N; BmPE36; immediate-early gene.
Bombyx mori nucleopolyhedrovirus
Bombyx mori nucleopolyhedrovirus
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'isolate="BmNPV-N9"
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                                                                                                                                                                                                                                                                                                              complement (5854. .6387)
/db xref="GI:30269988"
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Location/Qualifiers
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Faculty of Agriculture
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 78.3%;
Matches 123; Conservative
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Nagoya, Aichi 464-01
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NELRTIQIKQQRAMAELKKEPVINNFKFECSVCFETYSQQSNDTCPFLIPTTCHGFCF
KCVIDLQSNAMNIPHSIVCCPLCNTQVKAWRSLKPNAVVTCKFYKKTQERVPAVQQYK
NIIKVLQERSYISVENNDKNCDINMENQAKIVALEAELKTEKNHSDQYTSENRQLTEE
NTRLNEQVQELQRQVFTLRPQRGTTVNPQIGRDSAPAELNERFRSLAYSTISELFIE
NRVHSIQNYYYAGTSGAASSCDVNVTVNFGFEN"
1827. .1832
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                                                                                                                                                                                      /translation="MPRETNNRRHRSTPYERPTLEDLHROLEDALERRYOTRRRORO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 TTTTTTGCAATACAAAAAGTTCGCCTATGTTTGACATTTAATATACAGTACGAACTCTA 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 CAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACTATACGCTCTCAATATACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 CGTTTCGTAGACTATTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92; DB 14;
Pred. No. 5.3e-18;
0; Mismatches 45
                                                                                                                                /protein_id="BAA03364.1"
/db_xref="GI:222186"
     complement (487. .493)
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                                                                                /codon_start=1
/product="BmPE36"
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ilarity 72.6%;
Conservative 0
                                                           1776
TATA_signal
TATA_signal
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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May 10, 2005, 01:20:43 ; Search time 616.764 Seconds (without alignments) 5413.313 Million cell updates/sec Run on:

US-09-896-888A-1

Title: Perfect score:

1 catgatgataaacaatgtat.....tgttacagcgacacatg Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

8780412 Total number of hits satisfying chosen parameters: 4390206 segs, 2959870667 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* Database :

geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\*

geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2004as:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:\*

## SUMMARIES

|               |       | dР             |                          |    |          |                     |
|---------------|-------|----------------|--------------------------|----|----------|---------------------|
| Result<br>No. | Score | Query<br>Match | Query<br>Match Length DB | DB | ID       | Description         |
| 1             | 564   | 100.0          | 564                      | ~  | AAV62487 | Aav62487 O. pseudo  |
| 7             | 548   | 97.2           | 260                      | 12 | ADQ48575 | Adq48575 OpIE2 pro  |
| m             | 548   | 97.2           | 2773                     | σ  | AAL61306 | Aal61306 p2ZOp2F e  |
| 4             | 546.4 | 96.9           | 5038                     | 12 | ADQ48539 | Adq48539 Viral vec  |
| C)            | 101.4 | 18.0           | 279                      | N  | AAT13730 | Aat13730 AcNPV ORF  |
| 9             | 101.4 | 18.0           | 133894                   | ~  | AAT13635 | Aat13635 AcNPV qen  |
| 7             | 93.4  | 16.6           | 28413                    | 10 | ADC51646 | Adc51646 BmNPV ger  |
| 80            | 62    | 11.0           | 141                      | 12 | ADQ48576 | Adq48576 Viral vec  |
| υ<br>0        | 39.6  | 7.0            | 6289                     | œ  | ABZ10059 | Abz10059 Haematopo  |
| c 10          | 39.6  | 7.0            | 9289                     | 4  | AAS46501 | Aas46501 Tumour su  |
| c 11          | 39.6  | 7.0            |                          | 2  | ADE84121 | Ade84121 Human lym  |
| c 12          | 38    | 6.7            | 6289                     | æ  | ABZ10205 | Abz10205 Haematopo  |
| c 13          | 38    | 6.7            | 9289                     | 10 | ADE84197 | Ade84197 Human Iym  |
| c 14          | 36.2  | 6.4            | 2000                     | æ  | ADA71938 | Ada71938 Rice gene. |
| c 15          | 35.4  | 6.3            | 986                      | 9  | ABQ68715 | Abq68715 Listeria   |
| c 16          | 35.4  | 6.3            | 1549                     | 9  | ABQ70339 |                     |
| 17            | 34.4  | 6.1            | 855                      | 7  | AAV34232 | Aav34232 Human sec  |
| . 18          | 34.4  | 6.1            | 855                      | œ  | ACD08103 | Acd08103 cDNA enco  |
| 19            | 34    | 9.9            | 18977                    | 4  | ABL19380 | Abl19380 Drosophil  |
| c 20          | 33.8  | 6.0            | 1991                     | 9  | AAS18541 | Aas18541 Partial g  |
|               |       |                |                          |    |          |                     |

|   | Adh3400 Human col<br>Ab193815 Arabidops<br>Aac37066 Arabidops<br>Aac36504 Arabidops<br>Abc17343 Arabidops<br>Ada6882 Arabidops<br>Ada70711 Rice gene<br>Ad137609 Human ova<br>Ad127470 Human ova<br>Ad127470 Human HPP<br>Ab118801 Drosophil<br>Ab127502 Drosophil<br>Ab127502 Drosophil<br>Ab118800 Drosophil |
|---|--|
| ACN44823<br>ABZ42667<br>AAC97304<br>ACN43223<br>ACN43223<br>ACN4322<br>ABZ73951<br>ABZ73950<br>ABZ73950<br>ABZ73950<br>ABZ73950<br>ABZ73950<br>ABZ73950 | AAH30400 ABL93815 ABC93815 AAC37066 AAC37066 ABC77343 ADA70711 ADA9803 ABC18801 ABC27503 ABC17503 ABC18801   |
| 113<br>113<br>113<br>110<br>110<br>6  | ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~  |
| 2117<br>3056<br>3086<br>3203<br>3203<br>43053<br>43056<br>43056<br>14429<br>14429   | 426<br>111251<br>11251<br>1251<br>2000<br>2700<br>4780<br>4780<br>60604<br>11268<br>1368<br>3600   |
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## ALIGNMENTS

RESULT 1

O. pseudotsugata multicapsid nucleopolyhedrosis virus ie2 promoter. AAV62487 standard; DNA; 564 BP. (first entry) (revised) 17-OCT-2003 19-JAN-1999 AAV62487; AAV62487 

Orgyia pseudotsugata; multicapsid; nucleopolyhedrosis virus; opMNPV; Op ie2; promoter; shuttle vector; transformation; melanotransferrin; immediate early bacultovirus promoter; prokaryotic; transcription; bleomycin/phleomycin-type antibiotic; insect cell; transposon; ion transport peptide hormone; ss.

Orgyia pseudotsugata; polyhedrosis virus.

WO9844141-A2

08-OCT-1998

98WO-CA000282 26-MAR-1998; 97US-0049946P. 98CA-02221819. 27-MAR-1997; 28-JAN-1998; (UYBR-) UNIV BRITISH COLUMBIA.

Hegedus DD Theilmann DA, Pfeifer TA, Grigliatti TA,

WPI; 1998-557129/47.

Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins.

Claim 10; Page 82; 121pp; English.

This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis virus (OpMNPV) immediate early 2 (Op ie2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells

replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; OpIB2 promoter.

; 2002US-0396335P. ; 2002US-0398617P. ; 2002US-0427231P. ; 2003US-0456496P. ; 2003US-0474940P.

26-JUL-2002; 19-NOV-2002; 24-MAR-2003; 03-JUN-2003;

18-JUL-2002;

INVITROGEN CORP

(BENIN/)

18-JUL-2003; 2003WO-US022437

WO2004009768-A2

29-JAN-2004

Unidentified

site; recombinant virus;

promoter DNA sequence.

OpIE2 viral

vector;

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melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell lines from disparate species, allowing screening of lines for optimum post-translational modification of particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
              promoter having homology to, and capable of functioning as, an immediate early baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin/
phleomycin-type antibiotic under transcriptional control of (ii) and
(iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, useful to allow study of gene expression and direct expression of heterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 564; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.1e-172;
Matches 564; Conservative 0; Mismatches 0;
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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpIE2 promoter that was used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
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Pred. No. 1.8e-167;
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Best Local Similarity 100.0
Matches 548; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BENNETT R P.
WELCH P J.
HARWOOD S.
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FRIMPONG K.
FRANKE K E.
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ADQ48575 standard; DNA; 560

RESULT 2 ADQ48575 (first entry)

09-SEP-2004

ADQ48575;

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gene therapy. The present sequence is p2ZOp2F expression vector for insect cells. This sequence is used to illustrate the method of the
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                                    invention
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Matches !
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                                                      GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
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16-NOV-2001; 2001US-0331575P
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NIELSEN F S.
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                                              Length 2773;
Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
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                                         97.2%; Score 548; DB 9; Le
100.0%; Pred. No. 3.8e-167;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viral vector-related plasmid - pIB/V5-His-DEST.
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GGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGGGCGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 90-186; 122pp; English.
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NATU-) NATURAL ENVIRONMENT RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-IB000578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94GB-00013420
                                                                                                                                                          AAT13730/c
ID AAT13730 standard; DNA; 279
                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                         548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-087670/09.
                                                                                         CATCTGTT
                                                                                                                CATCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1995;
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06-SEP-1996
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                                                                                                                                                                                                                                                                     The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic arecombinant virus, generating replicates in prokaryotic dells. The nucleic acid of the invention defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful for producing and expression fusion polypeptides. The present DNA sequence represents a plasmid that was used in the
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                                                                                                                                                                                                    Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                           Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACAGGACGCCAGCTTCCTGTTGTTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCCACCAACTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCACTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 5038;
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96.9%; Score 546.4; DB 12
Best Local Similarity 99.8%; Pred. No. 1.7e-166;
Matches 547; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                  Example 18; Page 395-403; 555pp; English.
                                                                                                                                                           Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the invention
         26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                   CORP
                                                                                                                                                          Bennett RP, Welch PJ,
                                                                            BENNETT R P. WELCH P J. HARWOOD S.
                                                                                                                                                                                 WPI; 2004-132944/13.
                                                                                                            MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                   INVITROGEN
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(MADD/)
(FRIM/)
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AAT13636-731 show open reading frames 13, 20, 22-30, 32, 38, 41-46, 50-60, 62-63, 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-127, 129-130, 140 -146, 148-150, 152 and 154 from a total of 154 ORFs identified in the Autographa californica nuclear polyhedrosis virus (AcNPV) clone 6. Each gene is numbered according to its position in the virus genome beginning that left end of the linear map, and irrespective of its orientation. The direction of transcription is relative to that of the polyhedrin gene. Of the 154 ORFs identified it was found that some of the ORFs (ORFs 77, 30, 32, 71, 86, 123, 126 and 127) are dispensable for virus replication in cell culture or insect larvae. These genes can be deleted from the genome to: (a) provide additional sites for inserting single or multiple copies of foreign genes; and (b) to reduce the size of the virus complementary strand relative to the polyhedrin gene. The present sequence is designated ORF 152, and is on the complementary strand calative to the polyhedrin gene. (Updated on 16-OCT-2003 to standardise
480
                                                                                                                                                                                         540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector; baculovirus; ss.
                                                                                                                                                       GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
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/*tag= a
//under= ORF 152
//note= "corresponds to ACNPV nucleotides complement (132387-132109)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACNPV ORF 152, residues 132387-132109.
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132325

231

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Length 133894;

4.4e-21;

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132265 CTACAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACGATACGCTCCCAATATA 132265
                                                                                                                                          132384 AATTTTTTGCAATGCAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT
                                                                                                                                                                                                         172 CTACGTTCGTAGACTATTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                    132264 CTACTACACTATCAACTTTTTGCATTACAAAAAACTTCATTTTTGC 132218
                                                                                                                                                                                                                                                                                                             232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGC 278
Score 101.4; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BmNPV genomic DNA nucleotides 100001-128413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; silkworm; silkworm movement supression.
                   Pred. No. 4.46
0; Mismatches
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18.0%;
75.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 121; Conservative
                                                   Conservative
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                        Best Local Similarity
Matches 126; Conserv
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  Query Match
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                                                                                                                                                                                                           171
                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                              CTACAAATCGTAGACTATTTTTATTAGAATAGTCTACACTGTACGATACGCTCCCAATATA 157
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                                                                                                 DB 2; Length 279;
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                                                                                                    Score 101.4; DB 2; Length
Pred. No. 2.5e-22;
0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAAGTACGTGTCGGC
                                                0 U; 0 Other;
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                                                   A; 36 C; 68 G; 87 T;
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                                                                                                 Match 18.0%;
Local Similarity 75.4%;
tes 126; Conservative
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(first entry)
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                                                   BP; 88
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                                                   Sequence 279
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OS field)
                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231
                                                                                                                                                                                         The invention relates to a Bombyx mori (silk worm) polyhedrosis virus in which open reading frame 8 (ORP 8) gene is inactivated. The inactivated orfs gene is useful for suppressing movement of sulkworm and efficiently prevents the movement of a silkworm from a chamber in which it is raised. The present sequence is used in the exemplification of the invention.
mori polyhedrosis virus in which open reading frame gene is or its variant, useful for suppressing movement of Bombyx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22231 AATTTTTTGCAATACAAAAAGTTCGCCTATGTTTGACATATAATATACAGTACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28413 BP; 8394 A; 5713 C; 5940 G; 8366 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.6%; Score 93.4; DB 10; Length 28413; 72.5%; Pred. No. 8.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22111 CTACTACTATCAACTTTTTTGCATTACAAAAAGTTCATTTTTGC 22065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                  Claim 5; SEQ ID NO 3; 53pp; Japanese.
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Sequence 133894 BP; 39195 A; 27151 C; 27347 G; 40201 T; 0 U; 0 Other;

Haematopoietic cell proliferation disorder related DNA sequence #199.

(first entry)

16-JAN-2003

ABZ10059;

#1.

ABZ10059 standard; DNA; 6289 BP

62

61

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Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.

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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination. The presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The invention is also useful for producing and expressing fusion polypeptides. The was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                      viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid; recombination region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Franke KE;
                                                                                                                                     Viral vector-related plasmid pIB/V5-His-DEST recombination region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harwood S, Madden K, Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 62; DB 12;
100.0%; Pred. No. 1.2e-09
cive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 17; 555pp; English.
                                    ADQ48576 standard; DNA; 141 BP.
                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-03981TP.
19-NOV-2002; 2002US-042731P.
24-WAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0456496P.
                                                                                                                                                                                                                                                                                                                                           18-JUL-2003; 2003WO-US022437
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVITROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BENNETT R P.
WELCH P J.
HARWOOD S.
MADDEN K.
FRIMPONG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-132944/13.
                                                                                                                                                                                                                                                                        WO2004009768-A2
                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bennett RP,
                                                                                                     09-SEP-2004
                                                                                                                                                                                                                                                                                                         29-JAN-2004
                                                                    ADQ48576;
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(FRIM/) E
(FRAN/) E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WELC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BENN/)
RESULT 8
                     ADQ48576
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Pelet C;

Howe A, Mueller J; G, Lesche R, Leu E; Mueller V, Otto T, I

Guetig D, P, Grabs Model F,

Berlin K, Braun A, Distler J, Olek A, Piepenbrock C, Adorjan Lewin A, Lipscher E, Maier S,

(EPIG-) EPIGENOMICS AG

Lipscher E, N , Ziebarth H;

Lewin A, Li Schwope I,

WPI; 2003-018942/01.

26-MAR-2002; 2002WO-EP003401. 26-MAR-2001; 2001US-0278333P

WO200277272-A2 Homo sapiens.

03-OCT-2002.

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subject. The method comprises contacting a target mucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated cpG dinuclectides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention on be used: for invention on the present for disponce leaders from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder celated sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also subclasses, diagnosis, prognosis, treatment and/or monitoring of heamatopoietic cell proliferative method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6289 BP; 1680 A; 178 C; 1488 G; 2943 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 28; SEQ ID NO 199; 117pp; English.
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ö Gaps . . 74; Indels Score 39.6; DB Pred. No. 0.14; 0; Mismatches Local Similarity 53.2 tes 84; Conservative Matches

DB 8; Length 6289;

7.0%;

Query Match

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62; Conservative

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Local Similarity

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487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAAACACACAGTTGAACACACAGATCTG

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Gaps

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74;

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84; Conservative

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Local Similarity

Query Match Matches

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Score 39.6; Pred. No. 0.

7.0%;

DB 4;

0 U; 0 Other; Length 9289;

Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T;

7896 AATTTATTTATAAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 7837

172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA

231

1836 TAATAATTTTTAAAACATTATTATAAAAATCGTCACAATTCTTTTTACTCAAAAATA 7777

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4896 AATTTATTTATATAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 4837
                                                                                                                                                                                 4836 TAATAATTTTTÄAAACATTATTATÄÄÄÄÄÄÄTGGTCÄCAATTCTTTTTACTCAÄÄÄÄÄTÄ 4777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a speptide nucleic acid oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                              231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
                                                                                                           172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour suppressor gene derived chemically modified sequence #223
                                                                                                                                                                                                                                                                                                                          4776 ATACAACTTTCCTCTCCTATAAAACGAAAAAAAAA 4739
                                                                                                                                                                                                                                                       232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 223; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS46501 standard; DNA; 9289 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01033529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2001; 2001WO-EP002955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-602752/68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS46501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A,
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ID AAS46501/
AAS46501/
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The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between methylated and non-methylated CpG dinucleotides within the target nucleic acid. The genes and/or their regulatory regions are preferably selected from MDR1, CSMK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3, MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2B, FOS, GSK7D+1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C, GSK3Deta, ESR1, APAF1, BAK1, BAX or HOXAS. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders comprises contacting a target nucleic acid with at least or reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting and differentiating between lymphoid cell proliferative
                                                                                                                                                                                                           SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nimmrich I;
                                                                                                                                                   Human lymphoid cell proliferative disorder gene derived DNA #57
                                                                                                                                                                                       ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinucleotide; single nucleotide polymorphism; diffuse large B-cell lymphoms; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Becker E,
                                                                                                                                                                                                                                                                     follicular lymphoma; diagnosis; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; SEQ ID NO 117; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genc B,
                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
                                   ADE84121 standard; DNA; 9289
                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-2002; 2002WO-EP013265
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caldwell C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-457621/43.
                                                                                                                                                                                                                                                                                                                                            WO2003044226-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dinucleotides.
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                               29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders
                                                                           ADE84121;
RESULT 11
                   ADE84121,
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diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Note: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

```
Cpd dinucleotides within one or more the sequences, or their complements, for determining the cytosine methylation state and or single nucleotide polymorphisms (SNPs), and for differentiating at least two of the medical conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular differentiation between subclasses, diagnosis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence represents a nucleic acid of a pretreated genomic DNA derived from the
                                                                                                                                                                                                                                                                                                                                                 Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                above mentioned genes.
            884666666666888
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0
                                                                                              7896 AATTTATTTATAACCAAATAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 7837
                                                                                                                                                           7836 TAATAATITTTAAAACATTATTATAAAAATCGTCACAATTCTTTTTACTCAAAAATA 7777
                                                               231
                                                                                                                             172 CTACGITICGIAGACTATITIACATAAATAGICTACACCGITGTATACGCICCAAATACA
                                       Gaps
                                     ;
        Length 9289;
                                     Indels
                                                                                                                                                                                                                      7776 ATACAACTTTCCTCTCCTATAAAAACGAAAAAATA 7739
                                                                                                                                                                                          232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA 269
    Score 39.6; DB 10;
Pred. No. 0.16;
0; Mismatches 74;
      7.0%;
Query Match
Best Local Similarity 53.2
Matches 84; Conservative
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BP ABZ10205 standard; DNA; 6289 (first entry) 16-JAN-2003 ABZ10205; Ö RESULT 12

Haematopoietic cell proliferation disorder related DNA seguence #345. Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.

Ношо

WO200277272-A2.

03-OCT-2002.

26-MAR-2002; 2002WO-EP003401. 26-MAR-2001; 2001US-0278333P.

(EPIG-) EPIGENOMICS AG

Pelet C; Guetig D, Howe A, Mueller J; P, Grabs G, Lesche R, Leu E; Model F, Mueller V, Otto T, Berlin K, Braun A, Distler J, Olek A, Piepenbrock C, Adorjan Lewin A, Lipscher E, Maier S, Schwope I, Ziebarth H;

WPI; 2003-018942/01.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

Claim 28; SEQ ID NO 345; 117pp; English.

differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in subject. The method comprises contacting a target nucleic acid in a present invention describes a method for detecting and

dinuclectides within the target nucleic acid. AB209661 to AB21118
represent specifically claimed nucleotide sequences from the present
invention. Oligonuclectides from the present invention can be used:

differentiating between healthy haematopoietic cells and proliferative
disorder haematopoietic cells; for differentiating between acute
lymphocytic leukamia and acute myelogenous leukaemia; as probes for
determining the cytosine methylation state and/or single nucleotide
polymorphisms (SNPs) of haematopoietic cell proliferation disorder
related sequences and their complements; and as primers for the
amplification of haematopoietic cell proliferation disorder related DNA
sequences. The nucleotide sequences from the present invention can also
be used for detecting a predisposition to, differentiation between
cubel asses, diagnosis, prognosis, treatment and/or monitoring of
haematopoietic cell proliferative disorders. The present method enables a
highly specific classification of haematopoietic cell proliferative
disorders allowing for improved and informed treatment of patients ö 4896 AATTTATTTATATAAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 4837 171 4836 TAATAATTITITAAAACATTATTATAAAAATCATCACAATTCTTTTTACTCAAAAATA 4777 231 Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one 172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA Gaps ological sample obtained from the subject with at least 1 reagent, ds, lymphoid cell proliferative disorder; methylation; methylated Cpd dinucleotide; single nucleotide polymorphism; SNP; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma; Human lymphoid cell proliferative disorder gene derived DNA #133 ; Nimmrich distinguishes between methylated and non-methylated CpG Sequence 6289 BP; 1680 A; 0 C; 1488 G; 3121 T; 0 U; 0 Other; Length 6289; 75; Indels 4776 ATACAACTITCCTCTCCCTATAAAAAAAAAAAAAA 4739 Maier S, 232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA DB 8; 0.45; Score 38; DB 8 Pred. No. 0.45; 0; Mismatches Becker E, follicular lymphoma; diagnosis; prognosis. BP. 'n Genc / Match 6.7%; Local Similarity 52.5%; hes 83; Conservative ( ADE84197 standard; DNA; 9289 25-NOV-2002; 2002WO-EP013265 23-NOV-2001; 2001DE-01057491 28-DEC-2001; 2001DE-01064501 (first entry) ÅĞ. Caldwell C, WPI; 2003-457621/43. (EPIG-) EPIGENOMICS WO2003044226-A2 Homo sapiens 29-JAN-2004 30-MAY-2003 Burger M, ADE84197; Query Match which Matches RESULT 13 ADE84197/c g 셤 ò ò 셤 ò

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The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject by contacting at target nucleic acid in a biological sample obtained from the subject with methylated and non-methylated sample obtained from the subject with at least one reagent or series of reagents that distinguish between certain non-methylated and non-methylated sample obtained from the subject with and non-methylated sample of distinguish between certain The genes and/or their regulatory regions are preferably selected from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPID beta, MYDD1, CDH3, CDKN1B, CDKN1B, CDKN1B, CDKN1B, CDKN1C, GSTP1, HIC-1, MGMT, MLH1, MGS, MYC, PTEN, RBL2, TGFBR2, TGFR2B, FGS, GSTP1, HIC-1, MGMT, MLH1, MGS, MYC, PTEN, RBL2, TGFBR2, TGFN2B, CDKNIC, GSK3beta, ESR1, APAR1, BAX, BAX or HOXAS. Oligomers, peptide nucleic acid (FRA)-oligomers and/or isolated nucleic acids based on the sequences of the medical compliance (SNPs), and for differentiating stless two of the medical conditions such as diffuse large Ba-cell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular lymphocytic laweens subclasses, disaposis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence conditions acid of a pretreated genomic DNA derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7896 AATTTATTTATATATGCAAATAAAACTATTATAAATCCACTACCAAATATGATTCAAAAA 7837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant; bacterial infection; fungal infection; viral infection; rice;
reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 9289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9289 BP; 2515 A; 0 C; 2097 G; 4677 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 10; Length 92
Pred. No. 0.54;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7776 ATACAACTTTCCTCTCCCTATAAAAAAAAAAAAAA 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA 269
                                                         Claim 26; SEQ ID NO 193; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA71938 standard; DNA; 2000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105
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52.5%;
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Best Local Similarity 52.5
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     above mentioned genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003000898-A1.
                    dinucleotides.
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
                                                                                      t 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 WARSSGTWSRSAAKRTYKGYSTSRRAKMRACRMYSACRRYSRTSYYCGCSYCGSSKWKY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CTGCAAAAAACACGCTTTTGCACGCGGCCCATACATAGTACAAACTCTACGTTTCGTA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 MSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSMCCKKY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                  Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 RYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKOWKKSYYMSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 GACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 CSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYWYMSYMRYMMKCMCSRSCSSWMSCAYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; Listeria; food contamination; mutational analysis;
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Hou Y;
I, Zou (
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
Goff SA, Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 11.3%; Pred. No. 1;
Matches 42; Conservative 169; Mismatches 157;
 Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                         Claim 27; SEQ ID NO 5263; 899pp; English.
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ID ABQ68715 Btandard; DNA; 986 BP.
 Cooper B,
S, Tao Y,
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                                                                                                                                                                                                                                                                                                                                                                   illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 CCGCTTATCGC 494
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 Chang H, Chen W, Coo
Katagiri F, Quan S,
                                                  WPI; 2003-175290/17.
                                                                                                                                        gene expression
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29-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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(INSP ) INST PASTEUR. (CNRS ) CNRS CENT NAT RECH SCI.

Kunst F, Glaser P;

04-OCT-2001; 2001WO-FR003061 04-OCT-2000; 2000FR-00012697

WO200228891-A2. 11-APR-2002.

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ABOT1212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to pathogenicity of Listeria (potential therappeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wioo.int/pub/published_pot_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                         New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to nucleic acid sequences (ABQ67188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%; Score 35.4; DB 6; Length 986; Best Local Similarity 56.4%; Pred. No. 1.3; Matches 66; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 986 BP; 295 A; 199 C; 157 G; 328 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; SEQ ID NO 1528; 180pp; French.
                                                                                                                                                                                                                                                                                 WPI; 2002-332479/37
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155 CATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTG 214 318 cagartragaaaacarrrarcerreccaegaaaarrraaararcaaegaecacrererre 259 258 cagaacarrcararaaagrracarccarrcaarrrrrcggrgcrgragaggaag 202 215 TATACGCTCCAAATACACTACCACATTGAACCTTTTTGCAGTGCAAAAAGTACG 271 g ò ∂

0; Gaps

51; Indels

Search completed: May 10, 2005, 04:32:40 Job time : 623.764 secs

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36 GACGCCCAGCTTCCTGTGTTGCTAACCGCAGCCGAACGCAACTCCTTATCGGAACAGGACG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 GGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SRYRCHMSGKWCYSCCGYCCSACRMCYCWTRRMKSWYSSRKSRMCCRYMSMSSAYRYSSK
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Sequence 89, Appl
Sequence 1, Appli
Sequence 25113, A
Sequence 9827, Ap
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Sequence 16228, A
Sequence 12642, A
Sequence 13003, A
Sequence 13505, A
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Sequence 103864,
Sequence 103865,
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Sequence 103820,
Sequence 103821,
                                                                                   May 10, 2005, 04:19:16; Search time 187.525 Seconds (without alignments) 4921.273 Million cell updates/sec
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Sequence 160274,
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Sequence 160275,
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Sequence 86304
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

//cgn2_6/ptodata/1/ina/6B_COMB.seq:*

//cgn2_6/ptodata/1/ina/6A_COMB.seq:*

//cgn2_6/ptodata/1/ina/6B_COMB.seq:*

//cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

//cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-631-89-148-545-89

US-08-631-308-1

US-09-270-767-25113

US-09-249-016-103819

US-09-949-016-103819

US-09-949-016-103821

US-09-949-016-103865

US-09-949-016-103865

US-09-949-016-160231

US-09-949-016-160232

US-09-949-016-160232

US-09-949-016-160276

US-09-949-016-160278

US-09-949-016-160278

US-09-949-016-160278

US-09-949-016-13003

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Maximum Match 100%
Listing first 45 summaries
                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Perfect score:
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| 28 31 5.5 601 4 US-09-949-016-86306 Sequence 86306, A 30 31 5.5 601 4 US-09-949-016-86307 Sequence 86307, A 31 5.5 601 4 US-09-949-016-86308 Sequence 86307, A 32 31 5.5 601 4 US-09-949-016-86308 Sequence 86308, A 32 31 5.5 601 4 US-09-949-016-86309 Sequence 86310, A 33 31 5.5 7218 1 US-08-232-463-14 Sequence 14. Appl 34 31 5.5 7218 1 US-08-232-463-14 Sequence 14. Appl 35 31 5.5 74790 4 US-09-949-016-18321 Sequence 14182, A 4 US-09-949-016-18321 Sequence 14182, A 4 US-09-949-016-18321 Sequence 15321, A 5 170 4 US-09-949-016-18321 Sequence 11957, A 6 US-09-949-016-18321 Sequence 11957, A 6 US-09-949-016-18321 Sequence 11957, A 6 US-09-949-016-11357 Sequence 11957, A 6 US-09-949-016-11357 Sequence 11957, A 6 US-09-949-016-11357 Sequence 11957, A 6 US-09-949-016-11357 Sequence 11957, A 6 US-09-949-016-11270 Sequence 11957, A 6 US-09-949-016-11270 Sequence 11957, A 6 US-09-949-016-11270 Sequence 11957, A 6 US-09-949-016-11270 Sequence 11957, A 1 1 30.8 5.5 305491 4 US-09-949-016-11270 Sequence 17550, A 1 1 30.8 5.5 305491 4 US-09-981-17550 Sequence 17550, A 1 1 30.8 5.5 305491 4 US-09-981-17550 Sequence 17550, A 1 1 30.8 5.5 305491 4 US-09-981-17550 Sequence 17550, A 1 1 30.8 5.5 305491 4 US-09-981-1756 Sequence 17550, A 1 1 30.8 5.5 305491 4 US-09-981-1756 Sequence 17550, A 1 1 30.8 5.5 305491 4 US-09-981-1756 Sequence 11 3957, A 1 1 30.8 5.4 1 30.8 5.4 1 30.8 5.4 1 30.8 5.4 1 30.8 5.4 1 30.8 5.4 1 30.8 5.4 1 30.8 5.4 1 30.8 5.4 | RESULT 1  US-09-621-976-15639/c  Sequence 15639, Application US/09621976  Patent No. 6639063  GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Johnes Milne Edwards, J.B. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: FILE REFERENCE: GENES: 05.9PR. CURRENT FILING DATE: 2000-07-21  NUMBER OF SEQ ID NOS: 19335  SOFTWARE: Patent pm SEQ ID NO 15639  LENGTH: 505  TYPE: DNA  CORGANISM: Homo sapiens  US-09-621-976-15639 | 1.0%; Score 36.4; DB 4; 1.0%; Pred. No. 0.044; ve 159; Mismatches 165 crrrdcacgcgcccaracarag crrrgsskmrgkkgsmrkkkmmrrs aragrcracaccgrrgraracgcrc mmsgcwarsmkswarswysmwacw mmsgcwarsmkswarswysmwacw cgaaaaaagracgracacaccgc | ARMCRWMWSCRRMSYSCMG<br>ACGAGTGTTGTCTTATCGTG |
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| 01 01 01 01 01 01 01 01 01 01 01 01 01 0   | ו מונס בעוליייי לי מונס ו  | Query Best Best Matchu Matchu Oy Db Db   | oy oy                                       |

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FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11

APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/043,669

1997-04-11

FILING DATE: FILING DATE: FILING DATE:

60/043,312 60/043,313

1997-04-1

FILING DATE: 1997-04 APPLICATION NUMBER: APPLICATION NUMBER:

1997-04-1

1997-04-1

FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 PLICATION NUMBER: 60/043,315

FILING DATE:

APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877

1997-06-06

60/048,974

APPLICATION NUMBER:

FILING DATE:

1997-04-1997-04-

LING DATE:

60/026,889

FILING DATE: 1997-08-22

LICATION NUMBER:

APPLICATION NUMBER: 60/056,893 APPLICATION NUMBER: 60/056,630 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882

1997-08-2

FILING DATE:

DATE: 1997-08-22

FILING

1997-08-2

FILING DATE:

APPLICATION NUMBER: 60/056,903

FILING DATE: 1997-08-2; APPLICATION NUMBER: 60,

APPLICATION NUMBER: 60/056,637

1997-08-23

FILING DATE:

1997-08-22

FILING DATE:

FILING DATE: 1997-08-22

/056,888

APPLICATION NUMBER: 60/056,879

1997-08-23

FILING DATE:

APPLICATION NUMBER: 60/056,894

FILING DATE: 1997-08-22

FILING DATE: 1997-08-22

FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/

APPLICATION NUMBER: 60/056,911

1997-08-22

FILING DATE:

APPLICATION NUMBER: 60/056,636

1997-08-22

FILING DATE: FILING DATE: FILING DATE:

APPLICATION NUMBER: 60/056,874

APPLICATION NUMBER: 60/056,910

1997-08-2

60/056,864

PLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314

1997-04-1

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APPLICANT: Rosen et al.
IIILE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
                                                                                                                                                                                                                                FILING DATE: 1998-09-04
APPLICATION NUMBER: PCT/US98/04482
                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/148,545
                                                                                                                                                                                                                                                                  R FILING DATE: 1998-03-06
RR APPLICATION NUMBER: 60/040,162
RR FILING DATE: 1997-03-07
RR APPLICATION NUMBER: 60/040,333
ER FILING DATE: 1997-03-07
ER PILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                        A APPLICATION NUMBER: 60/040,161
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,626
R APPLICATION NUMBER: 60/040,334
R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,334
R FILING DATE: 1997-03-07
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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NG DATE: 1997-05-23
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FILING DATE: 1997-05-23
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TILING DATE: 1997-05-23
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ATE: 1997-05-23
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FILING DATE: 1997-05-23
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CATION NUMBER: 60/047,598
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CATION NUMBER: 60/047,613
IG DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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                                                                                         Sequence 89, Application US/09148545
Patent No. 6590075
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LING DATE: 1997-08-22 PLICATION NUMBER: 60/056,845 LING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,892

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2939 AAATAATGTTTGGTGGAAATGTTCATTAAACATCATTACAAATTTAATGAAAAGCATGC 2880
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                                                                                                                                                                                                                                         NUCLEIC ACIDS,
AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/01808
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: WO PCT/FR95/00172
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D. Julie K.
REGISTRATION NUMBER: 38 619
REFERENCE/DOCKET NUMBER: 38 619
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
                                                                                         APPLICANT: HABERT-CRIOLI, Estelle
APPLICANT: HABERT-CRIOLI, Estelle
APPLICANT: AMIRANOFP, Brigitte
APPLICANT: LOQUET, Isaballe
TITLE OF INVENTION: GALANIN RECEPTOR, NUC
TITLE OF INVENTION: TRANSFORMED CELLS AND
TORRESPONDENCES: 2
CORRESPONDENCES: 2
CORRESPONDENCES: 1
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
                                   Sequence 1, Application US/08693308 Patent No. 6447996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (610) 454-3839
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787..1836
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Best Local Similarity
Matches 68; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2819 CTAAA 2815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 60/043,501
EARLIER PILING DATE: 1997-04-13
EARLIER PILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/047,586

ER FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,590

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,594

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,599

ER FILING DATE: 1997-05-23

ER FILING DATE: 1997-05-23

ER PELING DATE: 1997-05-23

ER REPLICATION NUMBER: 60/047,593

ER REPLICATION NUMBER: 60/047,593

ER REPLICATION NUMBER: 60/047,593

ER REPLICATION NUMBER: 60/047,593

ER RELING DATE: 1997-05-23

ER RELING DATE: 1997-05-23

ER RELING DATE: 1997-04-11

ER RELING DATE: 1997-04-11

ER RELING DATE: 1997-04-11
                         R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/057,761

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

R PELING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R FLING DATE: 1997-05-23

R PLING DATE: 1997-05-23
ION NUMBER: 60/047,595
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TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1212 TAACTCGATGTAGCATCTCCAGATACAATTGAGCTCATAGAACTGTTTGAAAGGGGAAAAT 1153
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Sequence 9827, Application US/09270767

Sequence 9827, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NOWBER OF SEQ ID NOS: 62517

SEQ ID NO 9827

LENGTH: 5003
                                                                      GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 326-094
FILE REFERENCE: FILE REFERENCE: 18709/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25113
LENGTH: 902
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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US-09-270-767-25113/c
; Sequence 25113, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Drosophila melanogaster
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Best Local Similarity 56.4%;
Matches 62; Conservative
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-00-20

FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-00-09

FRIOR PILING DATE: 2000-00-09

NUMBER OF SEQ ID NOS: 207012

SSOCTHARE: FABESEQ for Windows Version 4.0

LENGTH: 601
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Sequence 103821, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYWORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 1.4;
0; Mismatches
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Pred. No. 1.4;
0; Mismatches
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PAPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
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; Sequence 103820, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 56.0
Matches 61; Conservative
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Best Local Similarity
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US-09-949-016-103820
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US-09-949-016-103865
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US-09-949-016-103865
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US-09-949-016-103864
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; Sequence 103663, Application US/09949016
; Rement No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOOD.307
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-0-09
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: RESECRED.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.7%; Score 32.2; DB 4; Length 601; Best Local Similarity 56.0%; Pred. No. 1.4; Matches 61; Conservative 0; Mismatches 48; Indels
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SOFTWARE: PASTES OF NIMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASTES OF WINDOWS VERSION 4.0
SEQ ID NO 103821
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US-09-949-016-103864
; Sequence 103864
; Parent No. 6812339
; GENERAL INFORMATION:
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Best Local Similarity
Matches 61, Conserva
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US-09-949-016-103821
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOC ID NO 103864

LENGTH: 601

LENGTH: 601
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Pred. No. 1.4;
0; Mismatches 48; Indels
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Pred. No. 1.
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Best Local Similarity 56.0%;
Matches 61; Conservative (
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Best Local Similarity 56.0°
Matches 61; Conservative
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US-09-949-016-160230
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Sequence 160274, Application US/09949016

Patent No. 6812339
GENERAL INPOWMATION:
TOTALE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 160274
                                                                     Sequence 160232, Application US/09949016
Fatent No. 681233
Fatent No. 681233
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR PAPLICATION NUMBER: 60/231,768
FRIOR PAPLICATION NUMBER: 60/231,498
FRIOR PAPLICATION NUMBER: 60/231,498
FRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Pred. No. 1.4;
0; Mismatches
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Pred. No. 1.4;
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Best Local Similarity
Matches 61; Conserv
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; ORGANISM: Human
US-09-949-016-160274
                                                        JS-09-949-016-160232
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ORGANISM: Human
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                 GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENENCE: CLOL1307

CURRENT APPLICATION NUMBER: 00/241, 755

PRIOR APPLICATION NUMBER: 60/231, 768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

FRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOFTWARE: FaetSEQ for Windows Version 4.0

LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: UNDER: 2000-04-14

PRIOR PLING DATE: 2000-04-02

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOTHARE: FABELSQ for Windows Version 4.0

LENGTH: 601
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Pred. No. 1.4;
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Sequence 160230, Application US/09949016
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Matches 61; Conservative
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Best Local Similarity 56.03
Matches 61; Conservative
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ORGANISM: Human
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Sequence

Title: Perfect score:

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Minimum DB Maximum DB

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100.0%; Score 564; DB 9; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.4e-175;
Matches 564; Conservative 0; Mismatches 0; Indels
7 US-10-221-714A-223

8 US-10-398-221-1528

1 US-10-398-221-3152

1 US-09-981-876-89

1 US-09-981-876-89

1 US-09-981-876-89

1 US-09-981-876-89

1 US-09-981-876-89

2 US-10-148-55-89

2 US-10-125-1463

3 US-10-10-192-1462

5 US-10-10-192-1462

8 US-10-10-192-1462

8 US-10-187-963-77138

1 US-09-770-444-580

1 US-09-770-444-580

1 US-09-938-842A-5148

1 US-09-938-842A-5148

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1 US-09-914-353-11499

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1 US-10-184-644-312

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US-10-198-846-11349
US-10-424-599-38274
US-10-424-599-101900
 17 US-10-221-714A-223
18 US-10-473-125-345
17 US-10-398-221-1528
17 US-10-398-221-1528
19 US-09-981-876-89
10 US-09-981-876-89
11 US-10-425-15-1041
13 US-10-425-15-1041
13 US-10-087-192-1462
13 US-10-087-192-1462
14 US-10-186-561
15 US-10-186-561
16 US-10-186-561
17 US-09-770-444-514
18 US-09-388-842A-514
18 US-09-388-842A-514
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18 US-09-814-353-1149
17 US-09-814-353-1149
17 US-10-351-951-1
17 US-10-351-951-1
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17 US-10-351-951-1
17 US-10-361-931-951-1
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18 US-10-156-761-1
18 US-10-156-761-1
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Sequence 1, Application US/0989688A

Sequence 1, Application US/0989688A

GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Innect Expression Vectors
FILE REPERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/048,911

PRIOR APPLICATION NUMBER: US/09/048,911

PRIOR PLILING DATE: 1998-03-26

PRIOR FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SEQ ID NO: SEQ ID NOS: 50

SEQ ID NO: SEQ ID NO: 2.0
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; ORGANISM: Orgyia pseudotsugata
US-09-896-888A-1
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Sequence 149, App
Sequence 16, Appl
Sequence 15, Appl
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Sequence 126, App
Sequence 60, Appl
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Sequence 89, Appl
Sequence 14, Appl
                                                                                                                  May 10, 2005, 05:52:55 ; Search time 1593.6 Seconds (without alignments) 2164.037 Million cell updates/sec
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                                                                                                                                                                                                                     1 catgatgataaacaatgtat......tgttacagcgacacaacatg
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/ cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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6 US-10-295-074-60

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US-09-896-888A-14

8 US-10-622-088-127

8 US-10-622-088-149

US-09-896-888A-15

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US-09-896-888A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
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seq length: 200000000
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Match Length
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2773
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Sequence 11, Appli Sequence 11, Appli Sequence 312, App Sequence 312, App Sequence 3538, Ap Sequence 2538, Ap Sequence 1, Appli Sequence 1, Appli

Sequence 1, Apply Sequence 11349, A Sequence 30372, A

Sequence 38274, A Sequence 55004, A Sequence 101900,

Sequence 345, App Sequence 1528, Ap Sequence 89, Appl Sequence 89, Appl Sequence 104158, Sequence 1463, App Sequence 125, App Sequence 125, App Sequence 2215, App Sequence 5148, App Sequence 512, App

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CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                245 ATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGCAGTCACGTAGGGCGGCCCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                                                                                                                                                            181 GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                                                                                                                                                                                        GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGGTTGTTGTCTTATCGT
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CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                            GGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC
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Publication No. US2030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmera A/S
TITLE OF INVERTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: p2ZOp2F expression vector for insect cells
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LOCATION: (561)...(566)
OTHER INFORMATION: HindIII site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (573)...(578)
OTHER INFORMATION: Aval site
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LOCATION: (586)...(591)
OTHER INFORMATION: ECORI site
FEATURE:
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                                                                                  GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAATACACTACCACAC
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              GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                      GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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APPLICANT: Madden, Knut
APPLICANT: Primpond, Kenneth
APPLICANT: Primpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
FILE REPERSINCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-16
PRIOR PILING DATE: 2002-07-16
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-07-16
PRIOR PILING DATE: 2003-07-64
PRIOR PILING DATE: 2003-07-64
PRIOR PILING DATE: 2003-07-64
PRIOR PILING DATE: 2003-07-64
PRIOR PILING DATE: 2003-03-64
PRIOR PILING DATE: 2003-06-03
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100.0%; Pred. No. 4.7e-170;
iive 0; Mismatches 0; Indels
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Sequence 126, Application US/10622088
Publication No. US20040219516A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 126
LENGTH: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J.
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ORGANISM: Unknown
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Matches 548;
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481 GICCCGCTTATCGCCCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 540
                              485 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 544
                                                                                                                                                                                  US-10-846-911-60

| Sequence 60, Application US/10846911
| Publication No. US20040258660A1
| GENERAL INFORMATION:
| APPLICANT: KIYSER, Steen
| APPLICANT: MISELSEN, Finn Stausholm
| APPLICANT: NOURLESEN, Finn Stausholm
| APPLICANT: WOLDBORG, Bjorn
| APPLICANT: WOLDBORG, Bjorn
| APPLICANT: WOUNDER, SOVEN
| TILLE OF INVENTION: NOVEL IMMUNGENIC MIMETICS OF MULTIMER PROTEINS
| FILE REFERENCE: 674542-2018
| CURRENT APPLICATION NUMBER: US/10/846,911
| CURRENT FILING DATE: 2004-05-14
| PRIOR FILING DATE: 2002-11-15
| PRIOR FILING DATE: 2001-11-16
| PRIOR FILING DATE: 2001-11-16
| PRIOR FILING DATE: 2001-11-16
| NUMBER OF SEQ ID NOS: 60
| SOFTWARE: Patentin version 3.1
| LENGTH: 2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (5867..(591)
OTHER INFORMATION: ECORI site
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NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
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LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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OTHER INFORMATION: Aval site
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OTHER INFORMATION: Clal site
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LOCATION: (573)..(578
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LOCATION: (629)..(634)
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100.0%; Pred. No. 1e-169;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
NAME/KEY: misc_recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
                                                                                                                                                                                                                                                        NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: ApalI site
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LOCATION: (2551)..(2556)

// OTHER INFORMATION: Apall site

US-10-295-074-60
                                                                                 NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: Clal site
                                                                                                                                               FEATURE:
NAME/KEY: misc_recomb
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.
Matches 548; Conservative
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Publication No. US20040219516A1
GENERAL INFORMATION:
APPLICANT: Benett, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942-5450007
CURRENT APPLICATION NUMBER: US/10/622,088
                                                                                                                                                                               Length 2773;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                        0;
                                                                                                                                                                              Query Match
97.2%; Score 548; DB 18;
Best Local Similarity 100.0%; Pred. No. 1e-169;
Matches 548; Conservative 0; Mismatches 0;
                                                    FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                    FEATURE:
NAME/KEY: misc recomb
LOCATION: (2551)..(2556)
COTHER INFORMATION: Apals site
US-10-846-911-60
                             LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
FEATURE:
NAME/KEY: misc_recomb
...mtoN: (2284)..(2285)
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US-10-622-088-89
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CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR PLICATION NUMBER: US 60/396,335
PRIOR PLILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR PLILING DATE: 2002-11-19
PRIOR PLILING DATE: 2002-11-19
PRIOR PLILING DATE: 2002-11-19
PRIOR PLILING DATE: 2003-14-19
PRIOR PLILING DATE: 2003-16-19
PRIOR PLILING DATE: 2003-06-06
PRIOR PLILING DATE: 2003-06-06
PRIOR PLILING DATE: 2003-06-06
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US-09-896-888A-14
Sequence 14, Application US/09896888A, Patent No. US20020116723A1
GENERAL INFORMATION:
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Matches 547; Conservative
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US-10-622-088-89
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2003-07-18
NUMBER: US 60/396,335
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Publication No. US20040219516A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
TITLE OF INVERTING: 0942: 5450007
FILE REFERENCE: 0942: 5450007
CURRENT PILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/10/622,088
PRIOR APPLICATION NUMBER: PCT/US03/22437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.9%; Score 462; DB 9; Length 462; 100.0%; Pred. No. 1.1e-141; tive 0; Mismatches 0; Indels
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APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44 CURRENT APPLICATION NUMBER: US/09/896,888A CURRENT FILING DATE: 2001-06-29 FRIOR APPLICATION NUMBER: US/09/048,911 PRIOR PILING DATE: 1998-03-26 PRIOR PILING DATE: 1998-03-26 PRIOR FILING DATE: 1997-03-27 NUMBER OF SEQ ID NOS: 50 SOFTWARE: PATENTIN NUMBER: 2001-03-27 SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 462; Conservative
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US-10-622-088-127
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1 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGATTGAACAGCATCTG 60
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APPLICANT: Madden, Knut
APPLICANT: Madden, Knut
APPLICANT: Framko, Kenneth
APPLICANT: Framko, Kenneth
CURRENT: Framko, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: US/10/622,088
FILE REFERENCE: 0942.545007
CURRENT FILING DATE: 2003-07-18
FRIOR APPLICATION NUMBER: PCT/US03/22437
FRIOR APPLICATION NUMBER: US 60/396,335
FRIOR APPLICATION NUMBER: US 60/396,17
FRIOR PRILING DATE: 2002-07-18
FRIOR PRILING DATE: 2002-07-26
FRIOR PRILING DATE: 2002-11-19
FRIOR FILING DATE: 2003-01-16
FRIOR APPLICATION NUMBER: US 60/427,231
FRIOR FILING DATE: 2003-01-16
FRIOR APPLICATION NUMBER: US 60/427,231
FRIOR FILING DATE: 2003-01-16
FRIOR SEQ ID NOS: 165
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 149
LENGTH: 325
THENDER PATENTIN VERSION 3.2
FROOFTWARE: PATENTIN VERSION 3.2
FROOFTWARE: PATENTIN VERSION 3.2
FROOFTWARE: PATENTIN VERSION 3.2
FROOFTWARE: PATENTIN VERSION 3.2
FROOFTWARE: PATENTIN VERSION 3.2
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FROOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Recombination region of pIB/VS-His-DEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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11.0%; Score 62; DB 18; I
Best Local Similarity 100.0%; Pred. No. 8.2e-10;
Matches 62; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

: LOCATION: (141)...(148)

: OTHER INFORMATION: n may be any nucleotide

US-10-622-088-127
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR FILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-06-03
PRIOR PILING DATE: 2003-06-03
PRIOR PILING DATE: 2003-06-03
PRIOR PILING DATE: 2003-06-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Description of Artificial Sequence: Fragment of CTHER INFORMATION: promoter sequence of the AcMNPV ien gene US-09-896-888A-16
                                                                                                                                                                                                                                   0
                                                                                                                                                                                          11.0%; Score 62; DB 18; Length 325;
100.0%; Pred. No. 1.2e-09;
ive 0; Mismatches 0; Indels
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Patent No. US20020116723A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TILE OF INVENTION: Insect Expression Vectors
FILE REPERSENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/896,888A

CURRENT FILING DATE: 2001-06-29

FRIOR APPLICATION NUMBER: US/09/048,911

PRIOR APPLICATION NUMBER: US/09/048,911

PRIOR APPLICATION NUMBER: US/09/048,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR PELING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 92
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Patent No. US20020116723A1
FEATURE:
NAME/KEY: misc_feature
LOCATION: (141). (142)
OTHER INFORMATION: n is a, c,
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Matches 62; Conservative
                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (145)..(276)
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                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Fragment of CTHER INFORMATION: promoter sequence of the AcMNPV ien gene US-09-896-888A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
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                                                                                                                                                                                                                                                                                                                            Query Match 7.6%; Score 42.6; DB 9; Length 8 Best Local Similarity 74.0%; Pred. No. 0.0016; Matches 54; Conservative 0; Mismatches 19; Indels
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Publication No. US20040048254A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 199, Application US/10473126; Publication No. US20040234973A1; GENERAL INFORMATION:
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Best Local Similarity 53.2%;
Matches 84; Conservative (
                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFFWARE: PatentIn Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 CTACGTTTCGTAG 184
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US-10-473-126-199/c
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LENGTH: 628
                                                                                                            LENGTH: 88
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155 CATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGGTTG 214
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                                                                                                                                                    Sequence 1528 Application US/10398221
; Publication No. US20040018514A1
; CENTERAL INFORMATION:
   APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; TILE OF INVENTION: Listeria innocua, genome and applications
; TILE REPERENCE: 344 702 - 08
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; PRIOR PILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: Patentin version 3.0
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; Publication No. U520040018514A1
; Publication No. U520040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST. Friedrik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 2003-03-27
; CURRENT FILING DATE: 2003-03-27
; PRIOR PLICATION NUMBER: PCT/FR 01/03 061
; PRIOR PLICATION NUMBER: FR 00/12 697
; PRIOR APPLICATION NUMBER: FR 00/12 697
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: Patentin version 3.0
; SOFTWARE: Patentin version 3.0
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NAME/KEY: misc feature

LOCATION: (1)...(end)

OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3152
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i OTHER INFORMATION: n can be any nucleotide a,g,c or t/u
US-10-398-221-1528
     4776 ATACAACTTTCCTCTCCTATAAAAAAAAAAAA 4739
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TYPE: DNA
ORGANISM: Listeria monocytogenes 4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Listeria monocytogenes-4B
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Best Local Similarity
                                                                                                                  RESULT 14
US-10-398-221-1528/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1836 TAATAATTTTTAAAACATTATTATAAAAAATCGTCACAATTCTTTTTACTCAAAAAAA 7177
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CURRENT APPLICATION NUMBER: US/10/221,714A

CURRENT FILING DATE: 2003-01-21

PRIOR PLICATION NUMBER: PCT/EPD1/02955

PRIOR PILING DATE: 2001-03-15

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| ATAAATAG        | <br>NATATCAAG   | CAGTGCAA   | <br>cggtgctg:  |
| TTTAC           | ATTTA   | TTTTC  | ATTTT  |
| TTTCGTAGACTA    |   | ACACATTGAACC   | Arccarrecrea   |
| CTACG           | TATCG   | CTACC  | GTTAC  |
| TACATAGTACAAACT |   | ATACGCTCCAAATACA   | 821 CAGAACATTCATATAAAGTTACATCCATCCTCAATTTTTCGCTGCTGTAGAGGAAG 765     |
| .55 CP          | 381 C   | 115 TZ   | 321 CP   |
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|                 | Qy 155 CATACATAGTACAAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGTTG 214 | OY 155 CATACATACTAAAACTCTACGTTTTCGTACATATTTTACATAAATAGTCTACACCGTTG 214 | Oy 155 CATACATAGTACAAACTCTAGGTTTCGTAGACTATTTACATAAATAGTCTACACCGTTG : |

Search completed: May 10, 2005, 10:28:53 Job time: 1600.6 secs

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|  | Pred.<br>score<br>and is  | Result<br>No. Sc        |                                    |  |   | un un                                 |                                      |   |                   |                  |                   | •                                    | 222                                    |                    | 52                | 27   | 7 7 8<br>7 8                                | 30                  | .,,   | ა დ<br>ა გ.                                | 3 3 2               | 37                 | 39 68                                    | ,                   | 1 27                                      | C 43 34 C 45 34   |

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100.0%; Pred. No. 5.7e-171;
tive 0; Mismatches 0;
US-09-048-911-1

Sequence 1, Application US/09048911

GENERAL INFORMATION:

APPLICAMT: The University of British Columbia

TITLE OF INVENTION: Insect Expression Vectors

FILE REPERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/048,911

CURRENT FILING DATE: 1998-03-26

SARLIER FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SEQ ID NO: SEQ ID NO: 2.0

LENGTH: 564
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GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REPERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888
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US-09-048-911-1
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Best Local Similarity 100.
Matches 564; Conservative
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US-09-896-888-1
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; LENGTH: 564
; TYPE: DNA
; ORGANISM: Orgyia pseudotsugata
US-09-896-8884-1
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PRIOR APPLICATION NUMBER: US 09/048,911
PRIOR FILING DATE: 198-03-26
PRIOR APPLICATION NUMBER: US 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
LENGTH: 564
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                                                                                                                               ; TYPE: DNA
; ORGANISM: Orgyia pseudotsugata
US-09-896-888-1
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US-09-896-888A-1
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FILE REFERENCE: 0942.545PC7
CURRENT APPLICATION NUMBER: PCT/US03/22437
CURRENT APPLICATION NUMBER: PCT/US03/22437
CURRENT PILLING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR PILLING DATE: 2002-07-26
PRIOR PILLING DATE: 2002-07-26
PRIOR PILLING DATE: 2002-07-26
PRIOR PILLING DATE: 2002-07-26
PRIOR PILLING DATE: 2003-03-24
PRIOR PILLING DATE: 2003-03-24
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PRIOR PILLING DATE: 2003-03-24
PRIOR PILLING DATE: 2003-05-03
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 126
LENGTH: 560
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        Length 564;
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; Pred. No. 5.7e-171;
0; Mismatches 0;
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Query Match
Best Local Similarity 100.
Matches 564; Conservative
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                                                                                                                                                         CATGATGATAAACAATGTTGGTGCTAATGTTGCTTCAACAATTCTGTTGAACTGTG 64
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US-10-622-088-126
i Sequence 126. Application US/10622088
i GENERAL INFORMATION:
i APPLICANT: Bennett, Robert P.
i APPLICANT: Welch, Peter J.
i APPLICANT: Madden, Knut
i APPLICANT: Frimpong, Kenneth E.
i APPLICANT: Franke, Renneth E.
i APPLICANT: Franke, Renneth E.
i TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
i CURRENT FILING DATE: 2003-07-18
i PRIOR FILING DATE: 2003-07-18
i PRIOR FILING DATE: 2003-07-18
i PRIOR FILING DATE: 2003-07-18
i PRIOR FILING DATE: 2003-07-18
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i PRIOR FILING DATE: 2002-07-18
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                                                                         Length 560
                                                                      97.2%; Score 548; DB 2; Length 56
100.0%; Pred. No. 8.6e-166;
ive 0; Mismatches 0; Indels
                          OTHER INFORMATION: OPIE2 promoter sequence
                                                                     Query Match
Best Local Similarity 100.
Matches 548; Conservative
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ORGANISM: Unknown
                                          PCT-US03-22437-126
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US-10-295-074-60
US-10-295-074-60
Sequence 60, Application US/10295074
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REPRENCE: PIOLI3DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT PILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOUTHWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 2773
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                                                                                                                                                                                                                                                                ; OTHER INFORMATION: OPIE2 promoter sequence US-10-622-088-126
                                                      60/474,940
PRIOR APPLICATION NUMBER: US 60/4
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/4
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin version 3.2
SEQ ID NO 126
LENGTH: 560
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                                                                                                                                                                                                                    ORGANISM: Unknown
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                                        305 GGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT 364
                                                                                                                                                                                     361 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 420
                                                                                                                                                                                                                                                                               421 GGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 480
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       365 GACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGCAACTCCTTATCGGAACA 424
                                                                                             301 GGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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APPLICANT: INVOCATION:

APPLICANT: RIKINSEN, Finn Stausholm
APPLICANT: BATT, Tomas

APPLICANT: BATT, Tomas

APPLICANT: BATT, Tomas

APPLICANT: BATT, TOMS

APPLICANT: WOLDBORG; Bion

TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

FILE REFERENCE: 674542-2018

CURRENT APPLICATION NUMBER: US/10/846,911

CURRENT APPLICATION NUMBER: PCT/DK02/00764

PRIOR PILING DATE: 2002-11-16

PRIOR APPLICATION NUMBER: 60/331,575

PRIOR APPLICATION NUMBER: 60/331,575

PRIOR PILING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn version 3.1

SEQ ID NO 60

LENGTH: 2773
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; Sequence 60, Application US/10846911
; GENERAL INFORMATION:
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NAME/KEY: misc recomb
LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
FEATURE:
NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
FEATURE:
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                                          OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.2%; Score 548; DB 51; Length 27 Best Local Similarity 100.0%; Pred. No. 1.7e-165; Matches 548; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc_recomb
LOAN:TON: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                   NAME/KEY: misc recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                                                        NAME/KEY: misc_recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
ORGANISM: Artificial sequence
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: ApalI site
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LOCATION: (2551).. (2556)
OTHER INFORMATION: ApaLI site
US-10-295-074-60
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LOCATION: (625)...(630)
OTHER INFORMATION: ClaI site
                                                                                                                                                                              NAME/KEY: misc recomb
LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (629)..(634)
OTHER INFORMATION: Clai site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.0%; Pred. No. 1.7e-165;
Matches 548; Conservative 0; Mismatches 0;
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NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
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NAME/KEY: misc_recomb
LOCATION: (2551)..(2556)
OTHER INFORMATION: Apali site
                                                            site
                                                                                                                                                                            NAME/KEY: misc recomb
LOCATION: (2284). (2289)
OTHER INFORMATION: Aval site
                                                                    FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: P&LI site
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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NAME/KEY: misc recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
FEATURE:
                                 NAME/KEY: misc recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apali
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GENERAL INVENTALION:

TITLE OF INVENTION: Viral Vectors Containing Recombination Sites

FILE REFREENCE: 0942.545PC07

CURRENT APPLICATION NUMBER: PCT/US03/22437

CURRENT APPLICATION NUMBER: PCT/US03/22437

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: US 60/396,617

PRIOR APPLICATION NUMBER: US 60/398,617

PRIOR PILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: US 60/427,231

PRIOR PLING DATE: 2002-11-19

PRIOR FILING DATE: 2003-01-496

PRIOR FILING DATE: 2003-03-44

PRIOR FILING DATE: 2003-06-03

NUMBER OF SEQ ID NOS: 146

SEQ ID NO 89

FEMALY. FALLY OF SEQ ID NOS: 146

SEQ ID NO 89
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Pred. No. 7.3e-165;
0; Mismatches 1;
PCT-US03-22437-89; Sequence 89, Application PC/TUS0322437; GENERAL INFORMATION:
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COTHER INFORMATION: pIB/V5-His-DEST
PCT-US03-22437-89
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Best Local Similarity 99.8%;
Matches 547; Conservative C
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Best Local Similarity 100.0%; Pred. No. 5.5e-138;
Matches 462; Conservative 0; Mismatches 0; Indels
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US-09-048-911-14

Sequence 14, Application US/09048911

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Insect Expression Vectors

FILE REPERBENCE: 80021-4

CURRENT APPLICATION NUMBER: US/09/048,911

CURRENT FILING DATE: 1998-03-26

EARLIER FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50
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US-09-896-888-14
Sequence 14, Application US/09896888
GENERAL INFORMATION:
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                                                                                                                       GENERAL INFORMATION;
APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Steven
APPLICANT: Madden, Knut
APPLICANT: Franke, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: PCT/US03/22437
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-11-19
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PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2003-01-18
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Pred. No. 7.3e-165;
0; Mismatches 1;
                                                                             ; Sequence 89, Application US/10622088; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.8%;
Matches 547; Conservative
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; OTHER INFORMA:
US-09-896-888A-14
           LENGTH: 46
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                   Length 462;
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Best Local Similarity 100.0%; Pred. No. 5.5e-138;
Matches 462; Conservative 0; Mismatches 0; Indels
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APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-4 CURRENT APPLICATION NUMBER: US/09/896,888 CURRENT FILING DATE: 2001-06-29 PRIOR PLICATION NUMBER: US 69/048,911 PRIOR PLICATION NUMBER: US 60/049,946 PRIOR FILING DATE: 1999-03-26 PRIOR FILING DATE: 1997-03-27 NUMBER OF SEQ ID NOS: 50 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0
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82-09-89-88A-14
; Sequence 14, Application US/0989688BA
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                          OTHER INFORMATION: Description of Artificial Sequence:Promoter OTHER INFORMATION: sequence of the OpMNFV ie2 gene
                                                                                                                                                 Length 462
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                                                                                                                                           81.9%; Score 462; DB 38; I
100.0%; Pred. No. 5.5e-138;
iive 0; Mismatches 0;
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                  Matches 462; Conservative
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SOFTWARE: Patentin version
SEQ ID NO 127
LENGTH: 147
                                                                                                                                               Query Match
Best Local Similarity
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PCT-US03-22437-127
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Application US/10622088
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                                                                                                                                                                                                                                                                                                        487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACACAGTTGAACAGCATCTG 546
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GENERAL INVORATION:
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Madden, Knut
APPLICANT: Franke, Wenneth
APPLICANT: Franke, Kenneth B.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: 0910.622,088
CURRENT APPLICATION NUMBER: PCT/US03/22437
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2003-07-18
PRIOR PRIOR DATE: 2002-07-26
PRIOR PLILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2002-11-19
PRIOR PLILING DATE: 2003-07-36
PRIOR PLILING DATE: 2003-07-36
PRIOR PLILING DATE: 2003-07-36
PRIOR PLILING DATE: 2003-07-36
PRIOR PLILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENT NOS: 165
PRIOR PLILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
PRIOR PLILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
PRIOR PLILING DATE: 2003-06-03
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                                                                                                                                                                  Query Match
11.0%; Score 62; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 62; Conservative 0; Mismatches 0; Indels
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; NAME/KEY: misc feature
; LOCATION: (141)...(148)
; OTHER INFORMATION: n may be any nucleotide
PCT-US03-22437-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 127, Application US/10622088 GENERAL INFORMATION:
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RESULT 15 US-10-622-088-149

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                                                     APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0922.5450007
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PLILNG DATE: 2002-07-26
PRIOR PLILNG DATE: 2002-07-26
PRIOR PLILNG DATE: 2002-07-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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11 Similarity 100.0%; Pred. No. 1.4e-08;
62; Conservative 0; Mismatches 0;
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NAME/KEY: misc_feature
LOCATION: (141)..(142)
OTHER INFORMATION: n is a, c, g, or
Harwood, Steven
Madden, Knut
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; LOCATION: (145)..(276)
US-10-622-088-149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 62; Conservi
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Sequence 2179, Ap
Sequence 6451, Ap
Sequence 6451, Ap
Sequence 24427, A
Sequence 1099, Ap
Sequence 2241, Ap
Sequence 25412, A
Sequence 25442, A
Sequence 3449, A
Sequence 3449, A
Sequence 3449, A
Sequence 25441, A
Sequence 15168, A
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Sequence 26311, A
Sequence 2178, Ap
Sequence 2179, Ap
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                                                                                                                                        May 10, 2005, 05:51:35 ; Search time 1390.39 Seconds (without alignments) 834.449 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

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4: /cgn2_6/ptodata/1/pna/USO7_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

12: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

13: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

13: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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|--|--|-------------------------------------|------------------------------------|--------------------------------------|------|------|------------------------------------|-------|----------------------------------|----------|----------------------------------|-------|--------------------------------|----------------------------------|-----------------------------------|------------------------------------|------|-------------------------------------|------|---------------------------------|--------------------------------|--------------------------------|------------------------------------|---------------|----------------------------------|------------------------------|
| 222<br>223<br>224<br>225<br>226<br>226<br>227<br>231<br>231<br>231<br>231<br>231<br>231<br>231<br>231  | 222<br>223<br>224<br>225<br>226<br>226<br>227<br>231<br>231<br>231<br>231<br>231<br>231<br>231<br>231  | 10                                  | 13                                 | 13                                   | 8    | æ    | 8                                  | 13    | ≓                                | 13       | Ξ                                | 11    | -                              | 13                               | 2                                 | 13                                 | σ    | σ                                   | 13   | œ                               | œ                              | ~                              | Ξ                                  | 2             | 11                               | 7                            |
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| 22222222222222222222222222222222222222   | 22222222222222222222222222222222222222   | 5.7                                 | 5.6                                | 9.9                                  | 9.9  | 9.9  | 9.9                                | 9.9   | 5.5                              | 5.5      | 5.5                              | 5.5   | 5.5                            | 5.5                              | 5.5                               | 5.4                                | 5.4  | 5.4                                 | 5.4  | 5.4                             | 5.4                            | 5.4                            | 5.4                                | 5.4           | 5.4                              | 5.4                          |
|  |  | 32.2                                | 31.6                               | 31.6                                 | 31.6 | 31.6 | 31.4                               | 31.4  | 31                               | . 31     | 31                               | 31    | 31                             | 31                               | 30.8                              | 30.6                               | 30.6 | 30.6                                | 30.6 | 30.6                            | 30.6                           | 30.6                           | 30.6                               | 30.6          | 30.6                             | 30.6                         |
| . , , , , , , , , , , , , , , , , , , ,  |  | 21                                  | 22                                 | 23                                   | 24   | 25   | 56                                 | 27    | 28                               | 59       | 30                               | 31    | 32                             | 33                               | 34                                | 35                                 | 36   | 37                                  | 38   | 39                              | 40                             | 41                             | 42                                 | 43            | 44                               | 45                           |
|  | •  | υ                                   |                                    |                                      | υ    | U    |                                    | υ     | υ                                | υ        |                                  | O     |                                | υ                                |                                   | υ                                  |      |                                     | ပ    | υ                               | ပ                              |                                |                                    |               |                                  |                              |

## ALIGNMENTS

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RESULT 1

US-10-199-107-60

Sequence 60, Application US/10939107

GERRELL INPORANTION:
APPLICANT: Beatr, Blank Rudolf
APPLICANT: Beatr, Blank Rudolf
APPLICANT: Beatr, Blank
APPLICANT: Beatr, Blank
APPLICANT: REMERNED: C14542-2020

FILE REPERRENCE: 674542-2020

CURRENT FILING DATE: 2004-09-10

FILE PERFERENCE: 6745-2020

CURRENT PILING DATE: 2004-09-10

FRIOR PELLING DATE: 2004-09-11

FRIOR FILING DATE: 2004-09-11

FRAUTE: NORMANION: PECOND

LOCATION: (5517). (556)

OTHER INFORMATION: Aval site

FRAUTE: NORMANION: BanHI site

FRAUTE: NORMANION: BanHI site

FRAUTE: NORMANION: BanHI site

FRAUTE: NORMANION: BanHI site

FRAUTE: NORMANION: BanHI site

FRAUTE: NORMANION: BanHI site

FRAUTE: NORMANION: BanHI site
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Woults, William Martin
APPLICANT: Woults, William Martin
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM.101083 (0.31896-042000)
CURRENT PALLICATION NUMBER: US/11/060,756
CURRENT PILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
PILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ATGATGATAAACAATGTATGTGCTAAATGTTGCTTCAACAACAATTCTGTTGAACTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 34; DB 10; Length 18977; ilarity 61.1%; Pred. No. 3.9; Conservative 0; Mismatches 35; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%; Score 33.8; DB 11; Length 600; 54.4%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-11-12
PRIOR PLILING DATE: 1999-11-12-8
PRIOR PLILING DATE: 1999-11-12
PRIOR PLILING DATE: 2090-01-12
PRIOR PLILING DATE: 2000-01-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26311
LENGTH: 18977
                                                                                                                            Sequence 26311, Application US/11097143 GENERAL INFORMATION:
                                                                                                                                                                           APPLICANT: Venter, J. Craig
         545 CATCTGTT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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Best Local Similarity
Trahes 55; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: DROSOPHILA
US-11-097-143-26311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                      US-11-097-143-26311
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CRGANISM: Homo
US-11-060-756-2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2178
LENGTH: 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CATGATGATAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG 64
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                    NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc recomb
LOCATION: (2551)..(2556)
OTHER INFORMATION: Apall site
                                                                                                                                                                                                                                  NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
                                          NAME/KEY: misc recomb
LOCATION: (629)...(634)
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                          LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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Best Local Similarity 100.
Matches 548; Conservative
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TITLE OF INVENTION: Mucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Target Genes TITLE REFERENCE: AMIO1083 (031896-042000) CURRENT APPLICATION NUMBER: US/11/060,756 CURRENT FILING DATE: 2005-02-18 NUMBER OF SEQ ID NOS: 303284 SOFTWARE: Patentin version 3.2 SEQ ID NO 6451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Avaion Pharmaceuticals
TITLE OF INVENTION: Determining Cancer-Linked Genes and Therapeutic Targets Using
TITLE OF INVENTION: Molecular Cytogenetic Methods
FILE REFERENCE: 689290-237
CURRENT APPLICATION NUMBER: PCT/USO5/07748
CURRENT FAPLICATION NUMBER: 60/550,304
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 3049
SOFTWARE: Patentin version 3.3
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                  469 AAATAATGTTTGGTGGAAATGTTCATTAAACATCATTACAAATTTAATGAAAAGCATGC 410
                                                                                                               70 TIGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTTGCACTGCAA 129
                                                                                                                                                       469 AAATAATGTTTGGTGGAAATGTTCATTAAACATCATTACAAATTTAATGAAAAAGCATGC 410
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                          10 AAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTGTTTTCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.0%; Score 33.8; DB Best Local Similarity 54.4%; Pred. No. 1.5; Matches 68; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                     US-11-060-756-6451/c;
Sequence 6451, Application US/11060756;
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application PC/TUS0507748 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-11-060-756-6451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                    349 CTAAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 CTAAA 345
                                                                                                                                                                                                       130 AAAAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 AAAAA 134
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PCT-US05-07748-6/c
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                                                                                                                                              음. 장
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                                                                                                                                                                                                                                                                                                                                                                                                  HAPPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Target Genes PILLE REPERENCE: AMIO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILLE DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
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                                                                       409 ATTIGIACAAGAIAGGAIACCCCAGGIAIATICAGICCCAIGAITITITIGAAIGICAI 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 TTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCAACAACTTTTTGCACTGCAA 129
                                               10 AAACAATGTATGGTGCTAATGTTGCTTCAACAATTCTGTTGAACTGTGTTTTCATGT
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  57; Indels
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54.4%; Pred. No. 1.5;
tive 0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match
6.0%; Score 33.8; Di
Best Local Similarity 54.4%; Pred. No. 1.5;
Matches 68; Conservative 0; Mismatches
  0; Mismatches
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US-11-060-756-6450/c
; Sequence 6450, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2179, Application US/11060756; GENERAL INFORMATION:
68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2179
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ORGANISM: Homo sapiens
US-11-060-756-6450
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Best Local Similarity
Matches 68; Conserva'
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US-11-060-756-2179/c
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                                                                                     2926 AAATAATGITTGGTGGAAATGITCATTAAACATCATTACAAATTTAATGAAAAAGCATGC 2867
                                                                                                                                                      70 TIGCCAACAAGCACCTITATACTCGGIGGCCTCCCCACCACCAACTITITGCACTGCAA 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETEROBERA INFESTATIONS TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF FILE REFERENCE: 38-21 (53885)
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                     57; Indels
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 54.4%; Pred. No. 2.6; tive 0; Mismatches
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6.0%; Score 33.6; Di
Best Local Similarity 66.7%; Pred. No. 2.3;
Matches 48; Conservative 0; Mismatches
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CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 26427
                                                                                                                                                                                                                                                                                                        Sequence 26427, Application US/60655875
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey
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; LOCATION: (1381)
; OTHER INFORMATION: n is a, c, g, or t
US-60-655-875-26427
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Miller, Nancy
Williams, Deryck
Vaudin, Mark
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Kovalic, David
Lu, Maolong
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LOCATION: (1051)..(1051)
OTHER INFORMATION: n is a,
                   68; Conservative
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Best Local Similarity
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US-10-472-963-1098
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APPLICANT:
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Sequence 1098, Application US/10472963
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS954PCT
CURRENT APPLICATION NUMBER: US/10/472,963
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: PCT/US02/09370

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APPLICANT: GALY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22475 CAACAACTCTTCTGTTCCATTGGGACTTTCAGTTCGTGAACCTCACCTTTTACAGTCTGT 22534
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TITLE OF INVENTION: Human Secreted Proteins
FILE REPERENCE: PS954PCT
CURRENT APPLICATION NUMBER: US/10/472,963
CURRENT FILING DATE: 2003-09-25
PRIOR PAPLICATION NUMBER: US/10/472,963
PRIOR FILING DATE: 2002-03-26
PRIOR PILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR SPILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 1834
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR PILING DATE: 2001-03-27
PRIOR PILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 1834
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1097, Application US/10472963; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.4%;
Matches 62; Conservative
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; ORGANISM: Homo sapiens
US-10-472-963-1098
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US-10-472-963-1097
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US-10-472-963-1097
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US-11-079-463-3281
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US-11-UJ/143-1495, Application US/11097143

Sequence 38495, Application US/11097143

GENERAL INFORMATION:
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DRESPHILA GENES.
TITLE OF INVENTION: DRESPHILA GENES.
TITLE OF INVENTION: DRESPHILA GENES.
TITLE OF INVENTION: DRESPHILA GENES.
TITLE OF INVENTION: DRESPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PLING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PLING DATE: 1999-10-19
PRIOR PELING DATE: 1999-10-19
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-2
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-03-24
PRIOR PELING DATE: 2000-03-24
PRIOR PELING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRACESQ for Windows Version 4.0
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51.4%; Pred. No. 5.4;
trive 0; Mismatches 71;
                                                                                  FRIOR FILLING DATE: 1999-10-19
PRIOR PELICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-2
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PASESEQ for Windows Version 4.0
SERICTH: 1268
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Best Local Similarity 51.4'
Matches 75; Conservative
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
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Pred. No. 5.3;
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0; Mismatches
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Pred. No. 5.3;
0; Mismatches
FILE REFERENCE: PATH00-03DIV2
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR PLING DATE: 1999-04-09
PRIOR PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 3281
LENGTH: 1221
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Best Local Similarity 55.39
Marches 63; Conservative
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US-11-079-045-3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: B.fragilis
US-11-079-463-3281
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Best Local Similarity
Matches 63; Conserv
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GENERAL INFORMATION:

APPLICANT: Venter, J. Craig
APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOO728

CURRENT APPLICATION NUMBER: 00/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR PELICATION NUMBER: 60/157,832

PRIOR PELICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PELING DATE: 1999-10-19

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-228

PRIOR PILING DATE: 1999-11-228

PRIOR PILING DATE: 1999-11-228

PRIOR PILING DATE: 1999-11-228

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-24

PRIOR PILING DATE: 2000-01-33

PRIOR PILING DATE: 2000-01-32

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Pred. No. 5.5;
0; Mismatches 71; Indels 0;
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Pred. No. 7.4;
0; Mismatches 71; Indels 0;
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211-097-143-38494/c
Sequence 38494, Application US/11097143
; GENERAL INFORMATION:
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Best Local Similarity 51.4%;
Matches 75; Conservative (
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Best Local Similarity 51.4%;
Matches 75; Conservative
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; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38495
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Run on: May 10, 2005, 03:45:00 ; Search time 3951.56 Seconds (without alignments) 5432.847 Million cell updates/sec

Title: US-09-896-888A-1
Perfect score: .564
Sequence: 1 catgatgataaacaatgtat.....tgttacagcgacacaacatg 564

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:\*
1: 9D-est1:\*
2: 9D est2:\*
3: 9D-htc:\*
4: 9D-est3:\*
5: 9D-est4:\*
6: 9D-est5:\*
7: 9D-9s81:\*
9: 9D-9s81:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|               |            |       | d              |                       |          |          |                    |
|---------------|------------|-------|----------------|-----------------------|----------|----------|--------------------|
| Result<br>No. | ult<br>No. | Score | Query<br>Match | Query<br>Match Length | DB       | ID       | Description        |
|               | 7          | 81.2  | 14.4           | 679                   | -        | AV398660 | AV398660 AV398660  |
|               | 7          | 39.6  | 7.0            | 954                   | 0        | CL077394 | CL077394 CH216-145 |
| υ             | m          | 39    | 6.9            | 762                   | σ        | BX147578 | BX147578 Danio rer |
|               | 4          | 39    | 6.9            | 1324                  | 6        | CG751412 | CG751412 P045-4-E0 |
| υ             | 'n         | 38.6  | 6.8            | 758                   | æ        | BH517933 | BH517933 BOGBL87TF |
|               | 9          | 38.2  | 6.8            | 535                   | 7        | N63392   | N63392 yz35h10.81  |
| υ             | 7          | 38    | 6.7            | 578                   | æ        | BZ902838 | BZ902838 CH240 23B |
|               | 80         | 38    | 6.7            | 582                   | ω        | BZ899636 | BZ899636 CH240 16P |
|               | σ          | 37.2  | 9.9            | 425                   | 9        | CB410241 | CB410241 NISC nc10 |
|               | 10         | 37.2  | 9.9            | 699                   | 7        | CO384338 | CO384338 AGENCOURT |
| υ             | 11         | 36.8  | 6.5            | 1101                  | σ        | CNS0039X | AL063938 Drosophil |
|               | 12         | 36.6  | 6.5            | 432                   | ٦        | AI437474 | AI437474 fb34b06.x |
|               | 13         | 36.6  | 6.5            | 580                   | 4        | BI843287 | BI843287 ft59f05.x |
| υ             | 14         | 36.6  | 6.5            | 1048                  | m        | CR709617 | CR709617 Tetraodon |
|               | 15         | 36.4  | 6.5            | 480                   | 9        | CB484581 | CB484581 ccluwtbh0 |
|               | 16         | 36.4  | 6.5            | 857                   | σ        | CG935894 | CG935894 MBEAVOSTR |
|               | 17         | 35.8  | 6.3            | 461                   | œ        | BH757407 | BH757407 SALK 0561 |
|               | 18         | 35.8  | 6.3            | 655                   | 0        | AG358704 | AG358704 Mus muscu |
|               | 19         | 35.8  | 6.3            | 675                   | 4        | BG695019 | BG695019 NISC iv11 |
|               | 20         | 35.8  | 6.3            | 715                   | 7        | BE374425 | BE374425 601227596 |
|               | 21         | 35.8  | 6.3            | 1049                  | δ        | CL510716 | CL510716 SAIL 836  |
| υ             | 22         | 35.6  | 6.3            | 516                   | 4        | BM278655 |                    |
|               | 23         | 35.6  | 6.3            | 613                   | σ        | CL753134 | CL753134 OR_BBa012 |
|               | 24         | 35.6  | 6.3            | 626                   | <u>.</u> | AG401197 | AG401197 Mus muscu |

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0; Gaps

9

129 AAAAAACACGCTTTTGCACGCGGCCCCATACATAGTACAAACTCTACGTTTCGTAGACTA 188

8 8

Query Match
14.4%; Score 81.2; DB 1; Length 679;
Best Local Similarity 71.3%; Pred. No. 2.1e-14;
Matches 107; Conservative 0; Mismatches 43; Indels

| 3a007     | 0110      | ogon      | 374 B    | - P00    | 3c055     | 122K2    | 59311    | phi1     | 2a09.    | กายตก    | phil     | A15D     | COURT     | ENTPMO1TF | CH213-86H | -886-    | retraodon  | 1315      | 6624      | 108.y     |
|-----------|-----------|-----------|----------|----------|-----------|----------|----------|----------|----------|----------|----------|----------|-----------|-----------|-----------|----------|------------|-----------|-----------|-----------|
| OR_BBa007 | nbeb00111 | Tetraodon |          | ZF101-P0 | ZMMBBc055 | NDL.122K | 60235931 | Drosophi | sak72a09 | Mus musc | Drosophi | IDOAAA15 | AGENCOUR' | ENTP      | _         | _        | •          | ISB1-13L5 | OST216624 | ut09a08.y |
| CL742215  | AQ857977  | AL188860  | AQ751255 | CK706618 | CG020891  | CC861440 | BG247625 | AL068607 | BM525801 | AG394612 | AL062985 | CN755468 | C0808859  | BH150387  | CL645025  | CE275017 | AL259808   | CL089685  | CG578872  | BE332182  |
|           |           |           |          |          |           |          |          |          |          |          |          |          |           |           |           |          |            |           |           |           |
|           |           |           |          |          |           |          |          |          |          |          |          |          |           |           |           |          |            |           |           |           |
| CL742215  | AQ857977  | CNS02APV  | AQ751255 | CK706618 | CG020891  | CC861440 | BG247625 | CNS00LO0 | BM525801 | AG394612 | CNS0067B | CN755468 | CO808859  | BH150387  | CL645025  | CE275017 | CNS 03 TGN | CL089685  | CG578872  | BE332182  |
| σ         | 8         | 6         | æ        | 7        | 6         | 6        | 4        | 0        | 4        | σ        | σ        | 7        | 7         | 8         | σ         | 6        | 0          | 6         | σ         | ~         |
| 665       | 787       | 1080      | 755      | 835      | 997       | 815      | 1019     | 1101     | 589      | 780      | 986      | 771      | 851       | 916       | 1275      | 717      | 892        | 1123      | 249       | 455       |
| 6.3       | 6.3       | 6.3       | 6.3      | 6.3      | 6.3       | 6.2      | 6.2      | 6.2      | 6.2      | 6.2      | 6.2      | 6.2      | 6.2       | 6.2       | 6.2       | 6.1      | 6.1        | 6.1       | 6.1       | 6.1       |
| 9.        | 9         | 9         | 4.       | 4.       | 4.        | N.       | 7        | ď        | 35       | 35       | 35       | ω.       | œ         | ω.        | ω.        | 9.       | 9.         | 9         | 4.        | 4.        |
| 35        | 35        | 35        | 35       | 35       | 35        | 35,      | 35       | 35       | •••      |          | 1-1      | 34       | 34.8      | 34        | 34        | 34       | 34         | 34        | 34        | 34        |
| 25        | 56        | 27        | 58       | 53       | 30        | 31       | 32       | 33       | 34       | 35       | 36       | 37       | 38        | 39        | 40        | 41       | 42         | 43        | 44        | 45        |
|           |           | U         | U        |          |           |          | U        |          | υ        | U        | U        | O        |           | O         | U         |          | υ          |           | U         |           |
|           |           |           |          |          |           |          |          |          |          |          |          |          |           |           |           |          |            |           |           |           |

## ALIGNMENTS

DEFINITION

RESULT 2 CL077394

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

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Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 109J14. 109J14 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida, Neodiplogasteridae, Pristionchus.

1 (bases 1 to 1324)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., yan der Muulen,M. and Sommer,R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG751412 1324 bp DNA linear GSS 24-OCT-2003 P045-4-E06.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 TACATAGTACAAACTCTACGTTTCGTAGACTATTTTTACATAAATAGTCTACACCGTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 TACGCTCCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  655 TÁTAAAATÁCACAAAATCCTATTAGTCGÁGCAÍTÍTTÁTTTÁÁTCGÍTTÍÁTÁGGAAAAAC
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommerætuebingen.mpg.de
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                            1 (bases 1 to 762)
Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 6.9%; Score 39; DB 9;
Best Local Similarity 56.7%; Pred. No. 0.71;
Matches 72; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .762
/organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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CG751412.1 GI:37973841
  BX147578.1 GI:27978953
                                                 Danio rerio (zebrafish)
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CH216-145B11 Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-145B11, genomic survey sequence.
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                                                 61 TITIATIAGAATAGTCTACACTGTACTATACGCTCTCAATATACTACTACTACACTATCAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus tropicalis (western clawed frog)

Renopus tropicalis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Renopodinae; Xenopus; Silurana.

(bases 1 to 954)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
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Danio rerio genomic clone DKEY-109J14, genomic survey sequence.
BX147578
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus tropicalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seg primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                    121 TTTTGATTACAAAAAGTTCATTTTGC 150
                                                                                                                        249 ITTTTGCAGTGCAAAAAGTACGTGTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 163
High quality sequence stop: 226.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Richard K Wilson
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Matches 87; Conserv
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FEATURES

RESULT 3 BX147578/c LOCUS DEFINITION ACCESSION

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N63392.1 GI:1211221
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N63392
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BOGBL87TF BOGB Brassica oleracea genomic clone BOGBL87, genomic
                                                                                                                                                                                                                                                                                        1092 AATATCACCACCTTTTTAATCTTTTTTTTTTTTTTCTGAAACCCCCTTTTTTAACCCTCC 1151
                                                                                                                                                                                                                                                                                                                                                            1152 TCCTTAGTAAACCCCAAAAGTTTGAATTCCATATACCGAGCCCTTTAAAATTAAACTCCA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea
Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                            GCCTCCCCACCACCAACTTTTTTGCACTGCAAAAAACACGCTTTTGCACGCGGGCCCAT 157
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                                                                                                                                                                                                                                                       AACAACAATTCTGTTGAACTGTGTTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTG
                                                                                                                                                                                                                                                                                                                                                                                              ACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTAT
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="pa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pHOS1; Site_1: BstX1; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstX1 linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 758)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea (Unpublished (2001)
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1272 regaaaaaaaacarrrrrccacccccararrrrrrrrccccaaaaagr 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 ACGCTCCAAATACACTACCACATTGAACCTTTTTGCAGTGCAAAAAGT 268
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Pred. No. 0.95;
0; Mismatches 79; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: FF
Class: sheared ends.
                                                                                                                                                                                     DB 9; Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                   Score 39; DB 9; Length 132
Pred. No. 0.81;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Brassica oleracea"
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/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="BOGB"
/note="Vector: pHOS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3712"
/clone="BOGBL87"
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                                                                                                                                                                                       Query Match 6.9%;
Best Local Similarity 48.1%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          survey sequence.
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Best Local Similarity
Matches 86; Conserva
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1 (Dases 1 to 515)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,Z., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Le,N.,
Mardia,B., Moore,B., Morris,M., Paragons,J., Prange,C., Rifkin,L.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 ATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGT 215
                                               468
                                                                                                                                                      467 CTCTACAAATTAATTAATACGATAAATTAATAAAAATAATAATGTATAAGGTTAATATA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: m13 -40 forward High quality sequence stop: 246.
                                                  527 CCAGTTGGTTTGCACTTTACAAGATTAATGATCAGTACTCTCATCAACAAATATTATAAA
                                                                                                       170 CTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                 N63392 . 535 bp mRNA linear EST
7235h10.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 38.2; DB 7; Length 535;
49.2%; Pred. No. 1.2;
tive 0; Mismatches 100; Indels (
                                                                                                                                                                                                           230 CACTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTGT 274
                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="GDB:3892208"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE: 285091 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:285091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
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REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Genome sequence
Contact: Harris Lewin
Contact: Harris Lewin
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana (L1801, USA)
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240 htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International BAC Mapping
Consortium (IBBMC) by by University of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG202-34480-11828
from USDA-CSREES and A099-32205-8534 from USDA/NRI (Livestock
Blate: 16 row: P column: 5
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 bp DNA linear GSS 12-JUN-2003 CH240 16PS.TV CHORI-240 Bos taurus genomic clone CH240_16PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Larkin, D.M., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A.
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                                                                                                                                                  61 TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT 120
                                                                                                                                                                                                                                                    192 TTTACCAAGCTTTTAAACACCACATTTATGTTTTGGGCCTAAATCATCAGCAAATGAATT 133
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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/clone_lib="CHOR1-240"
/note="Vector: pTARBAC1.3; Site_1: Mbol; Site_2: Mbol;
Hereford blomino 99375; GHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                            252 CATGCTGATCAATGAGGCATAAAGATATAATTGGTTTATAGACACATTTGTTGGAATGTA
                                                                                       1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                    Gaps
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        Similarity 55.2%; Pred. No. 1.4; 74; Conservative 0; Mismatches
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Pred. No. 1.4;
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_16P5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequence
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  Best Local Similarity
Matches 74; Conserv
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BZ899636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  578 bp DNA linear GSS 12-JUN-2003 CH240 23B3. TJ CHORI-240 Bos taurus genomic clone CH240_23B3, propries survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Wonnack,J.E., de Jong,P.J. and Lewin,H. With Cattle BAC-ends and Human A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                                       275
276 GGCAGTCACGTAGGCCGGCCTTATCGGGTCGCGTCCTGTCACGTACGAATCACATTATCG 335
                                                                                                                                                                                                                                                  338 recharceginancenecriegearegritinecriaceaeceaeceaegriting 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                    ATACGCTCCAAATACACTACCACACTTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTC
                                                                                                                                       278 ATTTGCCCAAATTTCACCAGGTTTTACTTAAAAATTCTACCTTATGGGTAAATACCAGGC
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/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mbo
Hereford bull_Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_23B3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequence
Unpublished (2003)
Other_GSSs: CH240_23B3.TV
                                                                                                                                                                                                                                                                                                       336 GACCGGACGAGTGTTGT 352
                                                                                                                                                                                                                                                                                                                                                          GACNGGATAAATNATTT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BZ902838.1 GI:31627927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae; Bos.
1 (bases 1 to 578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
                                                                                    216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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VERSION
KEYWORDS
SOURCE
ORGANISM
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DB 8; Length 578;

ORIGIN

FEATURES

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/tissue type="dorsal blastopore lip"
/lab_host="Top10"
/lab_host="Top10"
/lab_host="Top10"
/clone lib="Blumberg Cho dorsal blastopore lip"
/clone lib="Blumberg Cho dorsal blastopore lip"
/note="Organ: embryo; Vector: pBluescript SK-; Site_l:
BCORI; Site_2: Xhol; Library was prepared from 50 ug of
total RNA by oligo-dT priming and ANV reverse
transcriptses. After addition of EcoRI linkers and
ECORI-Xhol digestion, the CDNA was size selected by
chromatography on Sepharose CL-4B columns and fractions
containing cDNAs larger than SOO by were ligated into
ECORI-Xhol-digested lambda ZAPII (UniZAP-XR) and packaged
in vitro. Average insert size is 1.4 kb. The original
library contained 6 x 106 recombinants, of which 3 x 106
were amplified and stored at -7.0 C in SM buffer containing
7% DMSO. 3 x 106 pfu were mass excised and the resulting
phagemids used to infect Top10F. References: Science 253,
196-196 and Methods in Molecular Blology 97, 555-574.
Additional sequences from this library have been deposited
under the name Xenopus laevis dorsal blastopore lip.
Library constructed by Bruce Blumberg (University of
                                                                                                                                                                                                                          EST 30-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actional Institutes of Health, Mammalian Gene Collection (MGC)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Lunpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Bruce Blumberg

CDNA Library Preparation: Blumberg

CDNA Library Preparation: Blumberg

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M. A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
  126 TTTTTGATGCAATATATTTGCCAAAAAAACTCAGCTTTTATTTTCCATTTTAAACAACTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                       CO384338 10-JUP 669 bp mRNA linear EST 30-JUP AGENCOURT 26189343 Blumberg Cho dorsal blastopore lip Xenopus laevis CDNA clone IMAGE:7297357 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   column: 11
                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Place: LLAMIS222 row: j column
High quality sequence stop: 534.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenopodinae; Xenopus; Xenopus.
                                                                                              186 caararrracaagcierr 203
                                                                                                                                                                                                                                                                                                                        CO384338.1 GI:49490161
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                                                   235 CCACACATTGAACCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="both"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.9
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis
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AUTHORS
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JOURNAL
COMMENT
                                                                                                                                                                    RESULT 10
CO384338
                                                                                                                                                                                                                                                                                                 ACCESSION
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KEYWORDS
SOURCE
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Clone distribution: NIZ-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: information plate: LLAM12849 row G column: 18
Seq primer: -21M13 forward primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                     CB410241 425 bp mRNÀ linear EST 24-MAR-2003
NISC_nc10d09.x1 COGENE 6E MAX Homo sapiens cDNA clone IMAGE:5776553
3', mRNA sequence.
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                                                                                                                                             TITICALGITIGCCAACAAGCACCITIAIACTCGGIGGCCTCCCCACCACCAACTITIT 120
                                                                                                                                                                                      .325 TITACCAAGCITTTAAACACCCACATTTATGTTTTGGGCCTAAATCATCAGCAAATGAATT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTTCCAAAAAGGAAAAAAATTTTTTTCCTCGGGGTTTTATCCACTGTCAATACTGTA 125
                                                                                    265 CATGCTGATCAATGAGCATAAAGATATAATTGGTTTAATGACACATTTGTTGGAATGTA 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
  Gaps
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  60; Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .425
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5776553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB410241.1 GI:29166981
                                                                                                                                                                                                                                                 121 GCACTGCAAAAAA 134
                                                                                                                                                                                                                                                                                            385 TCAGCATTAAAAA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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Matches 75; Conservative
74; Conservative
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                                                                                                                                               61
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TITLE
Matches
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KEYWORDS
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EST 07-JUN-2001

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sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                            Lark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="26 somite embryos, adult livers, shield stage embryos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1810
  A1437474 432 bp mRNA linear EST 07-:
ESSA Desix1 Zebrafish WashU MPIMG EST Danio rerio CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: zbrafish@watson.wustl.edu
                                                      IMAGE:3713747 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 423 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:3713747"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                        Danio rerio (zebrafish)
                                                                                                       AI437474.1 GI:4286113
                                                                                                                                                                               Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                            DEFINITION
                                                                                                                                                                          ORGANISM
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JOURNAL
COMMENT
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                                                                                                  VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                        1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACK8012 of RPCI-98 library from Drosophila melanogaster (fruit AL063938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  949
CCCATACATAGTACAAACTCTACGTTCGTAGACTATTTTACATAAATAGTCTACACGT 212
                                              104 CCAATAAATAGGGGAACCTTCTGGTATAGTTGTAAAGAATACATCCAATGTATGCAACGT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTTGCACTGCAAAAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AACACGCTTTTGCACGCGGGCCCATACTACTACAAACTCTACGTTTCGTAGACTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 1101)
                                                                                               213 TGTATACGCTCCAAATACACTACCACACTTGAACCTTTTTGCAGTGCAAAAAA 266
                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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/clone="BACR08012"
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/note="end : T7"
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/lab host="DH10B (phage-resistant)"
/clone lib="Gong zebrafish ovary"
/clone lib="Gong zebrafish ovary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
Site_1: Xho1; Site_2: EcoRI; Poly A+ RNA was isolatd from
the Ovaries of 2 female adult zebrafish (4-5 month old).
CDNAS were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagens) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
                                                                                                                                                                                                                                                                                                                   04-OCT-2001
                                                               ACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (Bases 1 to 580)
1 (Bases 1 to 580)
2 (Lark,M., Johnson,S.L., Lehrach,H., Lee,R., Lii,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,Es., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Wabu Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
                  Arcactriratriccracresegracascergaarrirtractrirecaaagreaaaacre 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
Seq primer: T7 from Gibco
High quality sequence Stop: 410.
                                                                                                          AGTGAACAATTTACAAATATATAAAACAACAACTGTTTTCTTTGGCTACTAAGCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                         ACACTACCACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGCA 279
                                                                                                                                                                                        141 ACTCTACTACACCTTCAATTACACGGAGAGCCTAAAAGTACATGACAGAA 191
                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                       580 bp mRNA linear EST
ft59f05.x1 Gong zebrafish ovary Danio rerio cDNA clone
INMAES157656 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
/mol_type="mRNA"
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Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
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Fax: 314 286 1810
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CB484581 480 bp mRNA linear EST '01-APR-2003 ccluwtbh009074 Coregonus clupeaformis head Coregonus clupeaformis cDA4, mRNA sequence.
CB484581. GI:29295807
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                                                 82 ACCTTTATACTCGGTGGCCTCCCCACCACCACTTTTTTGCACTGCAAAAAAACACGCTT 141
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Direct Submission

Submitted (10-A004) Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

More information available at

http://www.genoscope.cns.fr/tetraodon.

Location/Qualifiers
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Indels
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Tetraodon nigroviridis
Tetraodon nigroviridis
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84;
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Pred. No. 4.5;
0; Mismatches 95;
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  Mismatches
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/db_xref="taxon:99883"
/tissue_type="Eggs"
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Best Local Similarity 49.5%;
Matches 93; Conservative
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VERSION

DB 4; Length 580

Score 36.6; DE Pred. No. 3.9;

6.5%;

Query Match Best Local Similarity

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Coregonus.

(Dases 1 to 480)

GRASP Consortium, Davidson, W.S., Koop, B.F. and
http://web.uvic.ca/cb/grasp.

A Burvey of Salmo salar transcripts from high complexity cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Koop BF,
Contract: Koop BF,
Contract: Koop BF,
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
PI: 250 472 4067
Fax: 250 472 4067
Email: bkoop@uvic.ca
Email: bkoop@uvic.ca
Contract for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
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/note="Vector: pBlueScriptIISK+; Library Creator:
Kristian R von Schalburg ; Lake whitefish tissue
contributor: Louis Bernatchez (Universite Laval)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
6.5%; Score 36.4; DB 6; Length 480;
Best Local Similarity 51.9%; Pred. No. 4.4;
Matches 82; Conservative 0; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Coregonus clupeaformis"
/mol_type="mRNA"
/db_xref="taxon:59861"
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                               Coregonus clupeaformis
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Unpublished (2002)
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Db 130 CACTTGGGATATGCAAGCCATTTTACAGAAATGGACTA 167 Search completed: May 10, 2005, 07:25:08 Job time : 3957.56 secs

70 GACAAATTTTATGGTAAATATTAAGTCACAATTCAGCAACTGTATGCTTACTAATACAA 129

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169 ACTCTACGTTTCGTAGACTATTTTACATAATAGTCTA 206

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